

FIGURE 1

Find Neighbors  
and Assemble  
Flow Diagram

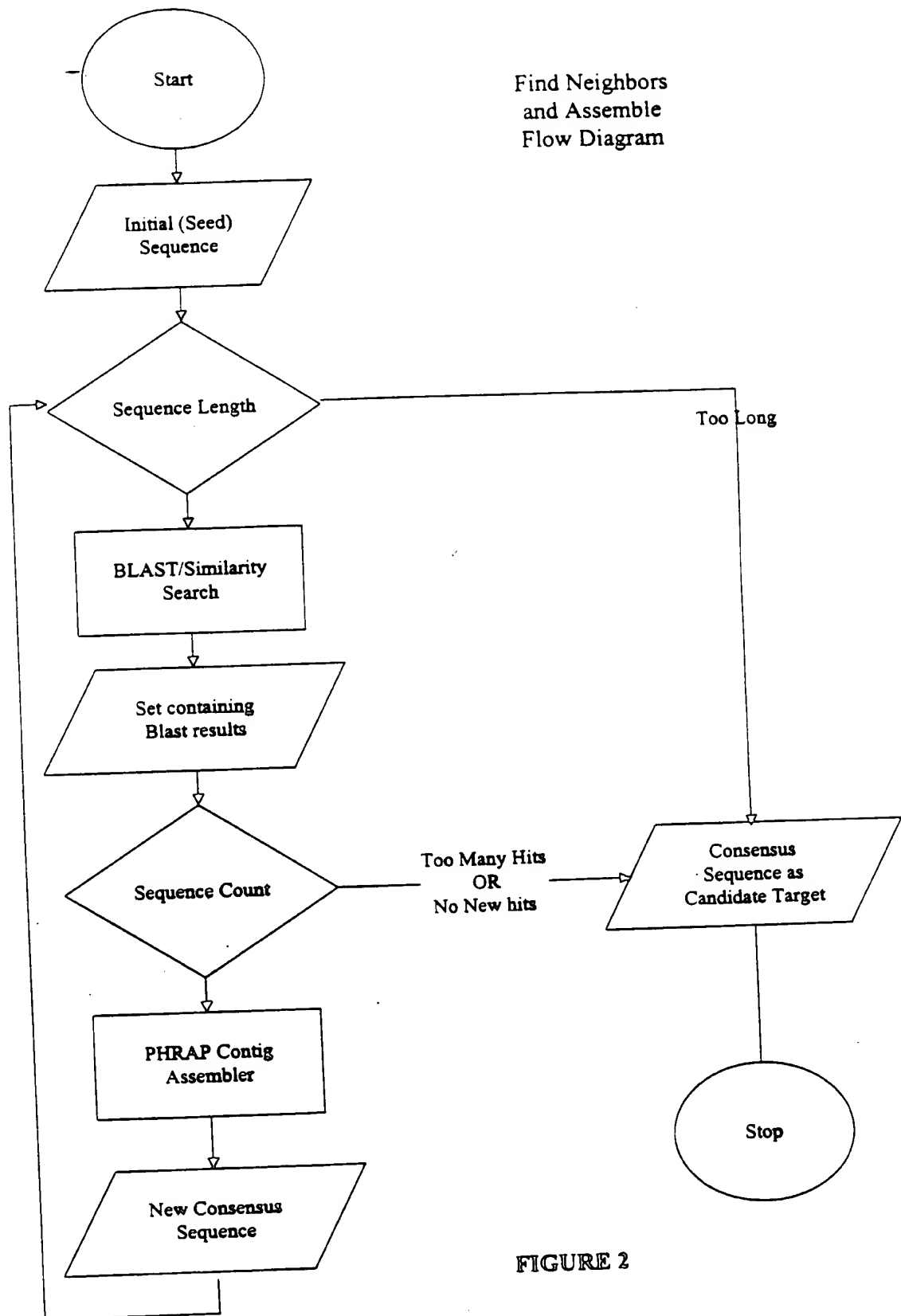


FIGURE 2

-BlastParse

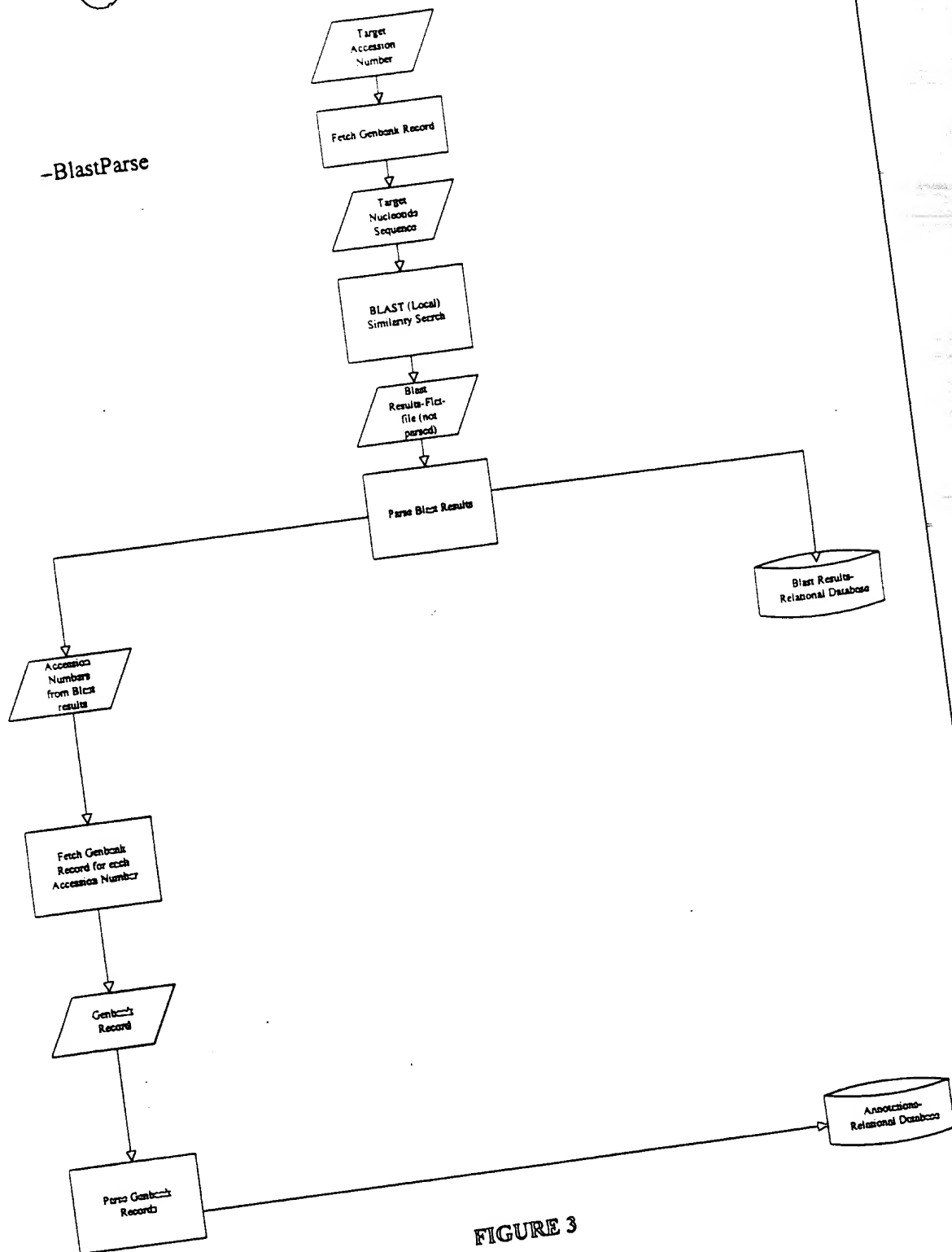


FIGURE 3

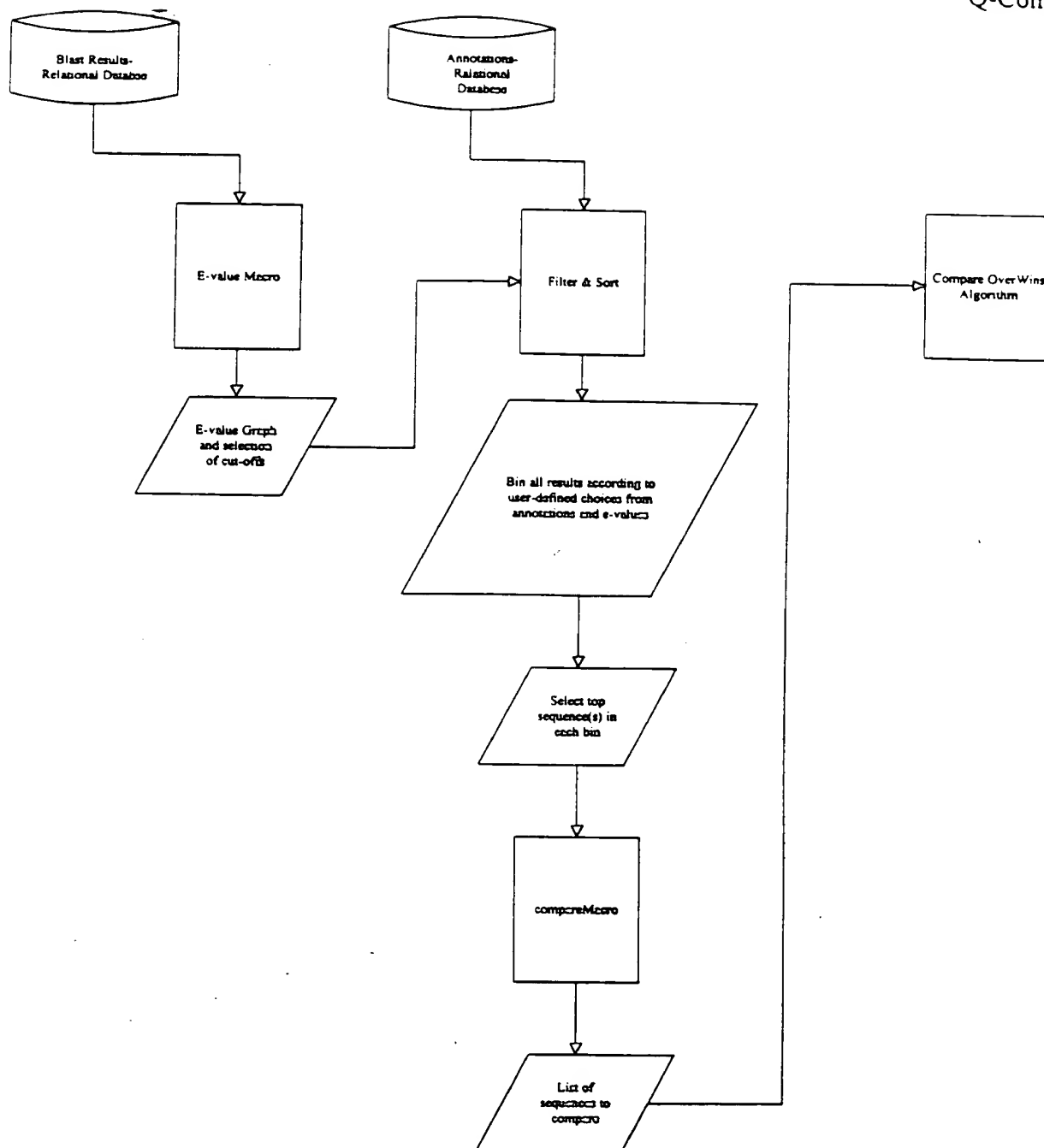


FIGURE 4



# CompareOverWins Algorithm Flow Chart

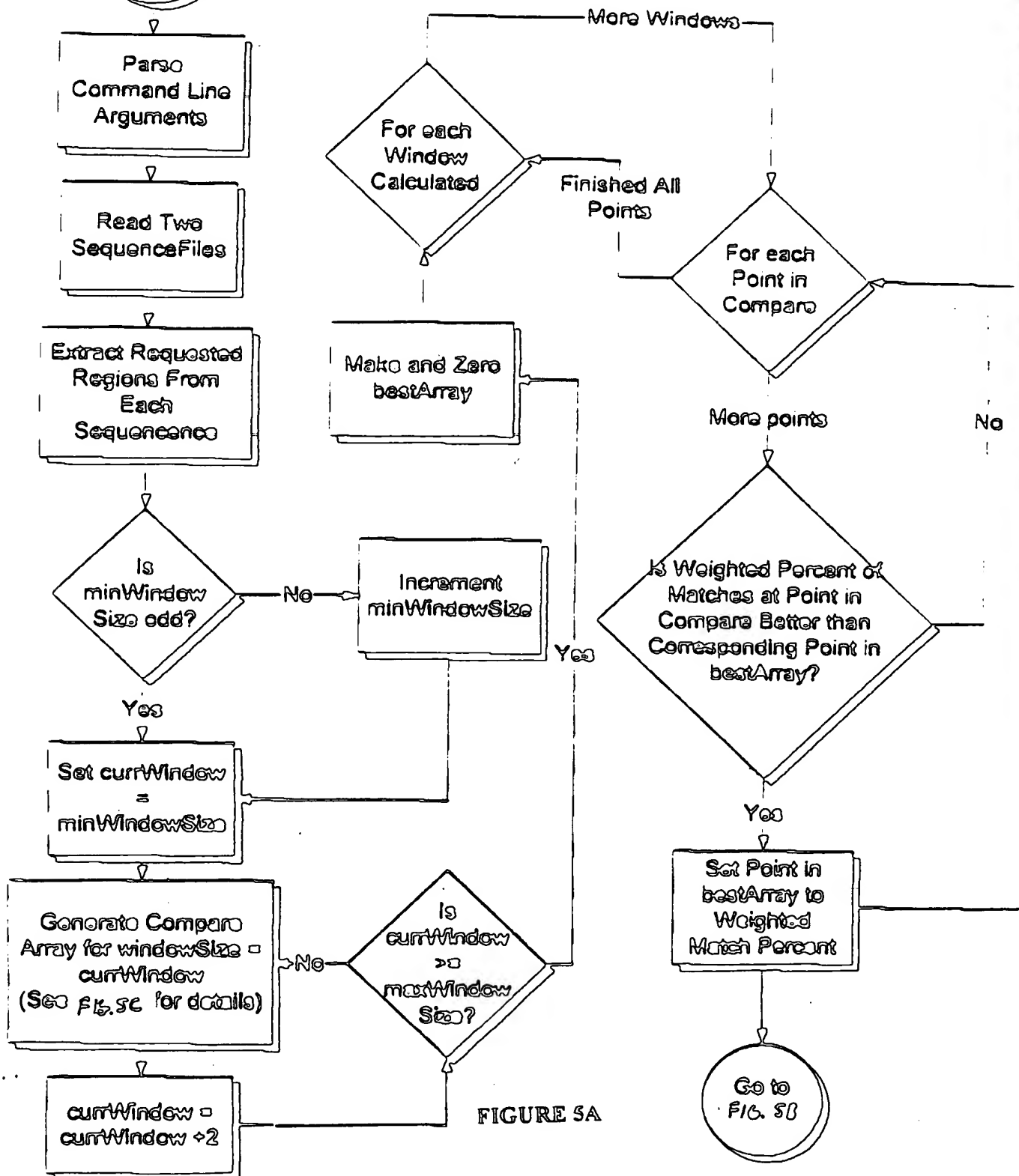
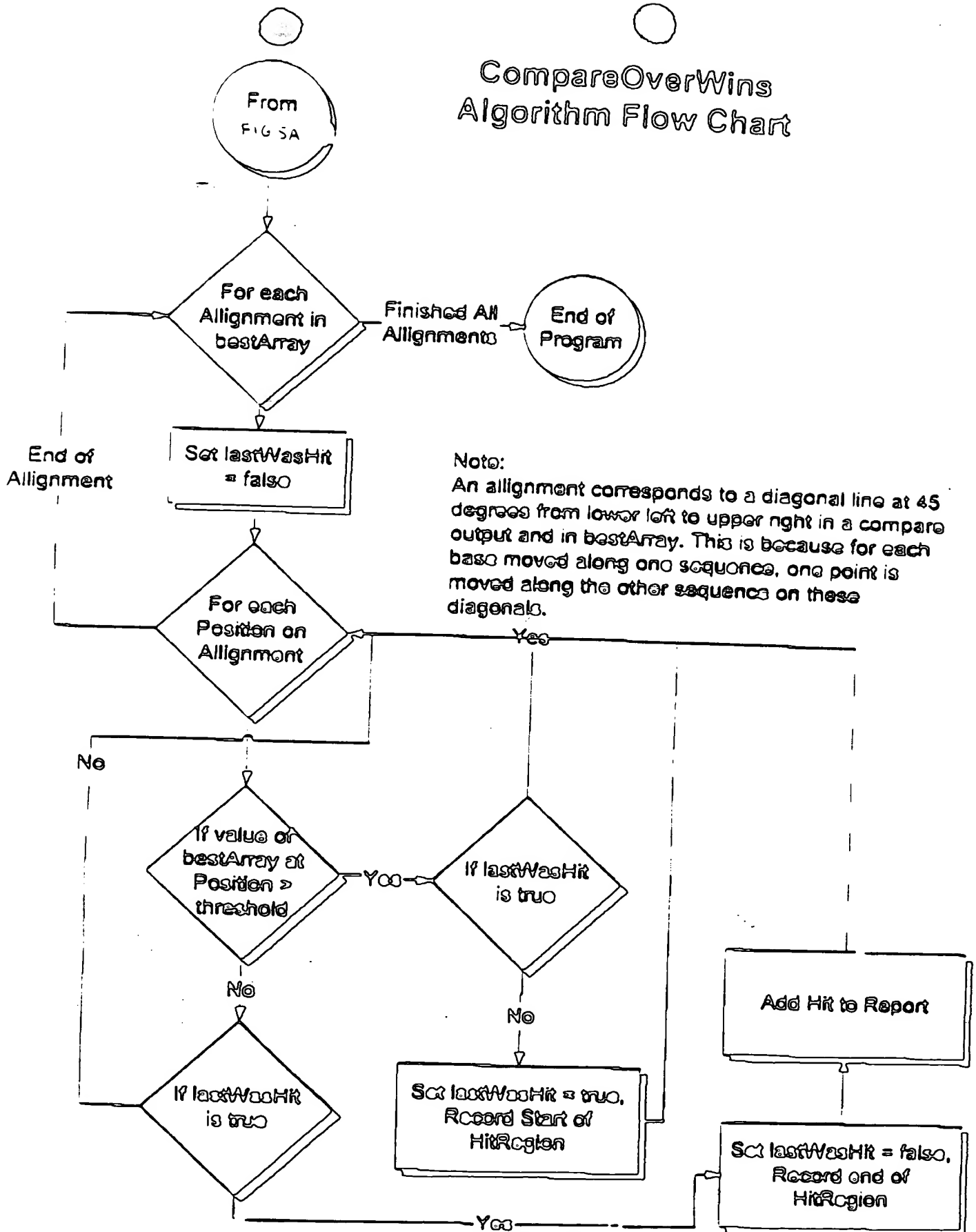


FIGURE 5A

# CompareOverWins Algorithm Flow Chart



# CompareOverWins Algorithm Flow Chart Basic Compare

Input:  
Sequence A length a  
Sequence B length b  
Window Size

Output:  
Array of size a by b of unsigned chars (0-255)  
Each point represents the number of matches in the window at that alignment and position

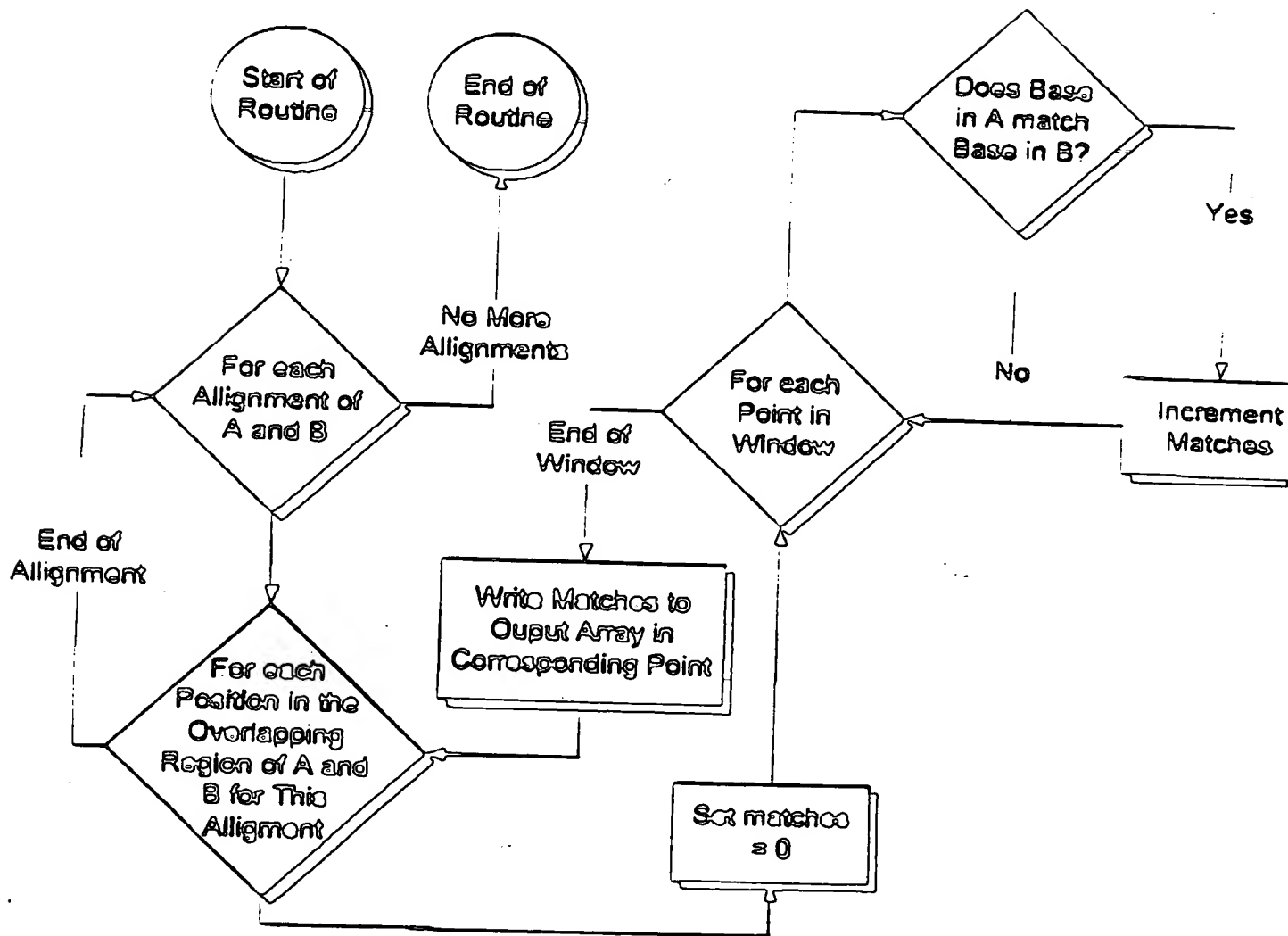
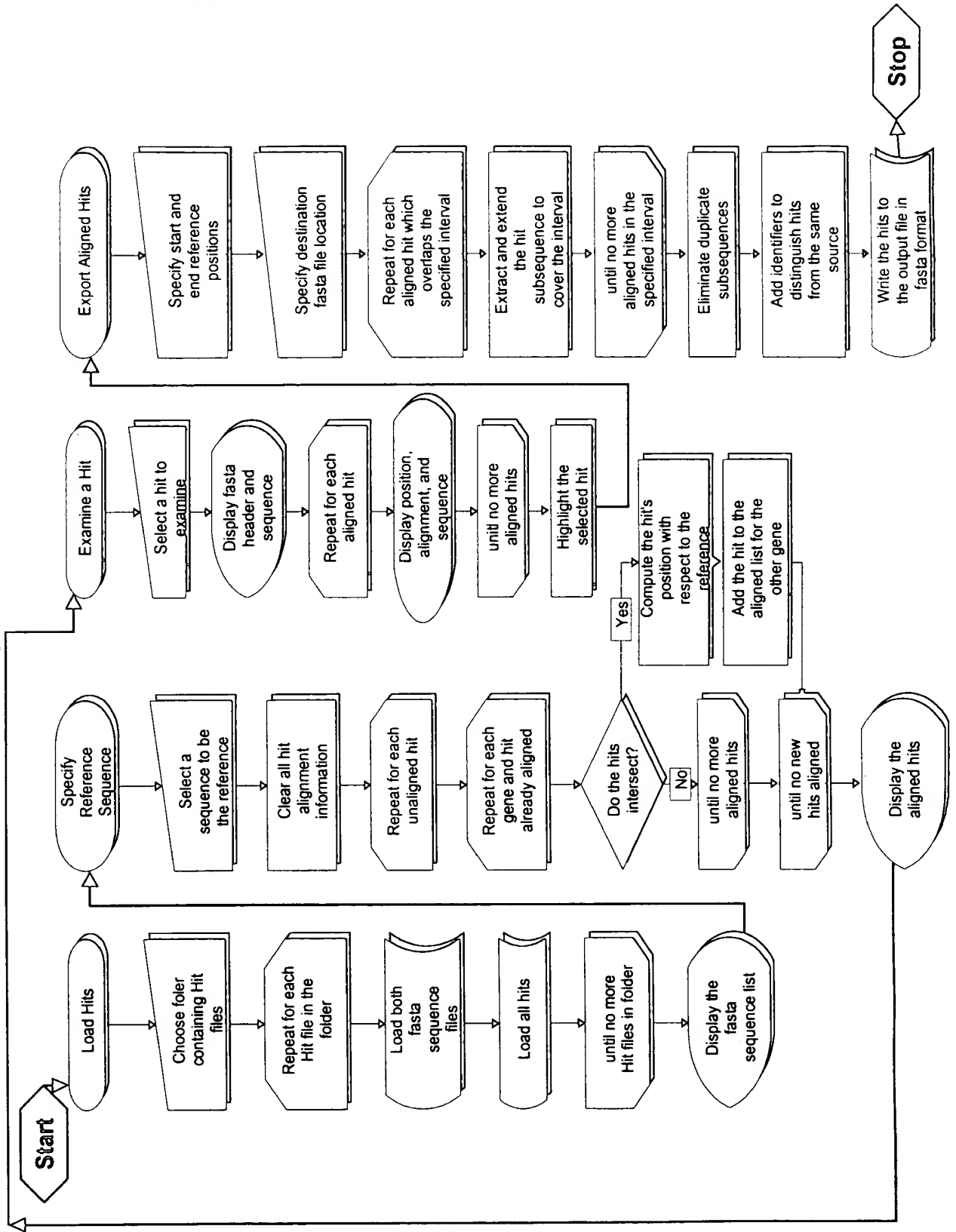
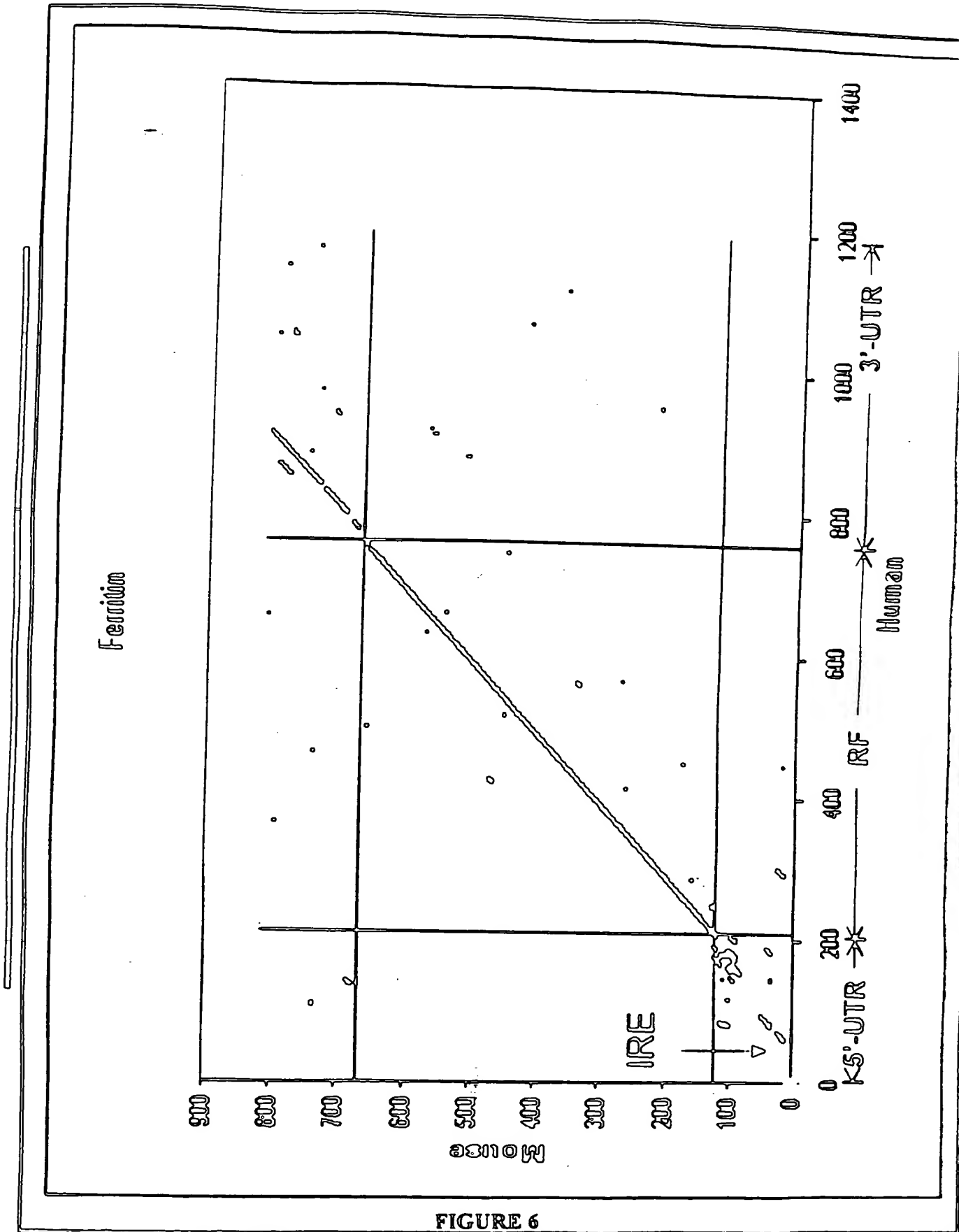


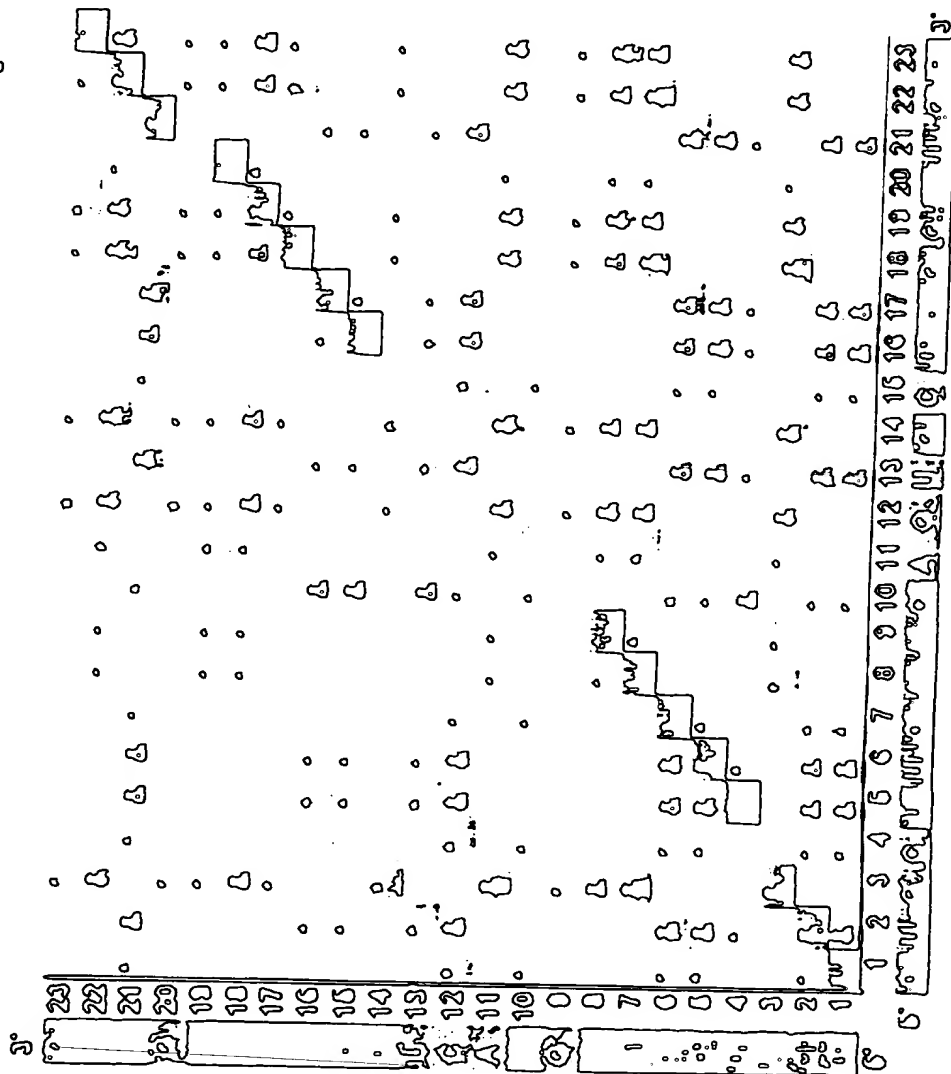
FIGURE 5C

Fig. 5D





# Self Complementation Analysis - Single Sequence



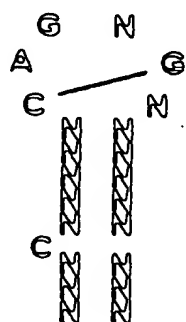
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23  
 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

FIGURE 7

[illegible]

## Typical Descriptor

This is an example of a descriptor used to identify iron response elements. To search the database using RNAMOT, the stem-loop model is converted to a text string as shown below:



IRE

Stem-loop  
Model

H1 S1 H2 S2 H2 H1

H1 3:3 NNN:NNN

S1 1 C

H2 5:5 NNNNN:NNNNN

S2 6 CAGNCG

W2

M0

IRE String descriptor

This descriptor allows for a wobble (W) of 2 (allows G-U pairing) and no mismatches. N can be any nucleotide. H refers to the stem region while S refers to the single stranded region.

FIGURE 9



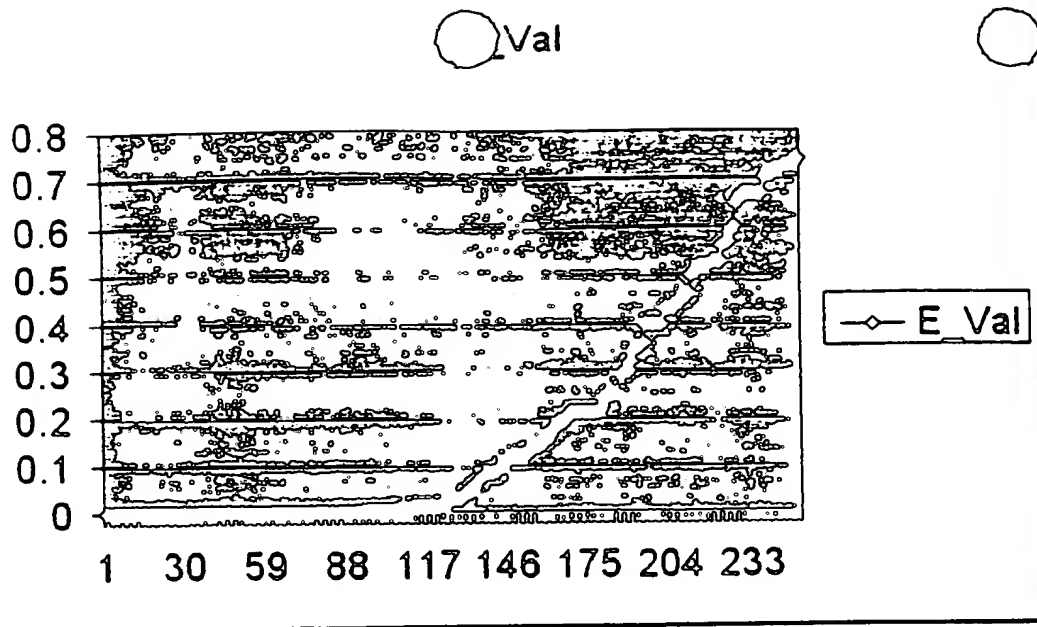


FIGURE 10

1000 900 800 700 600 500 400 300 200 100 0

Ferritin

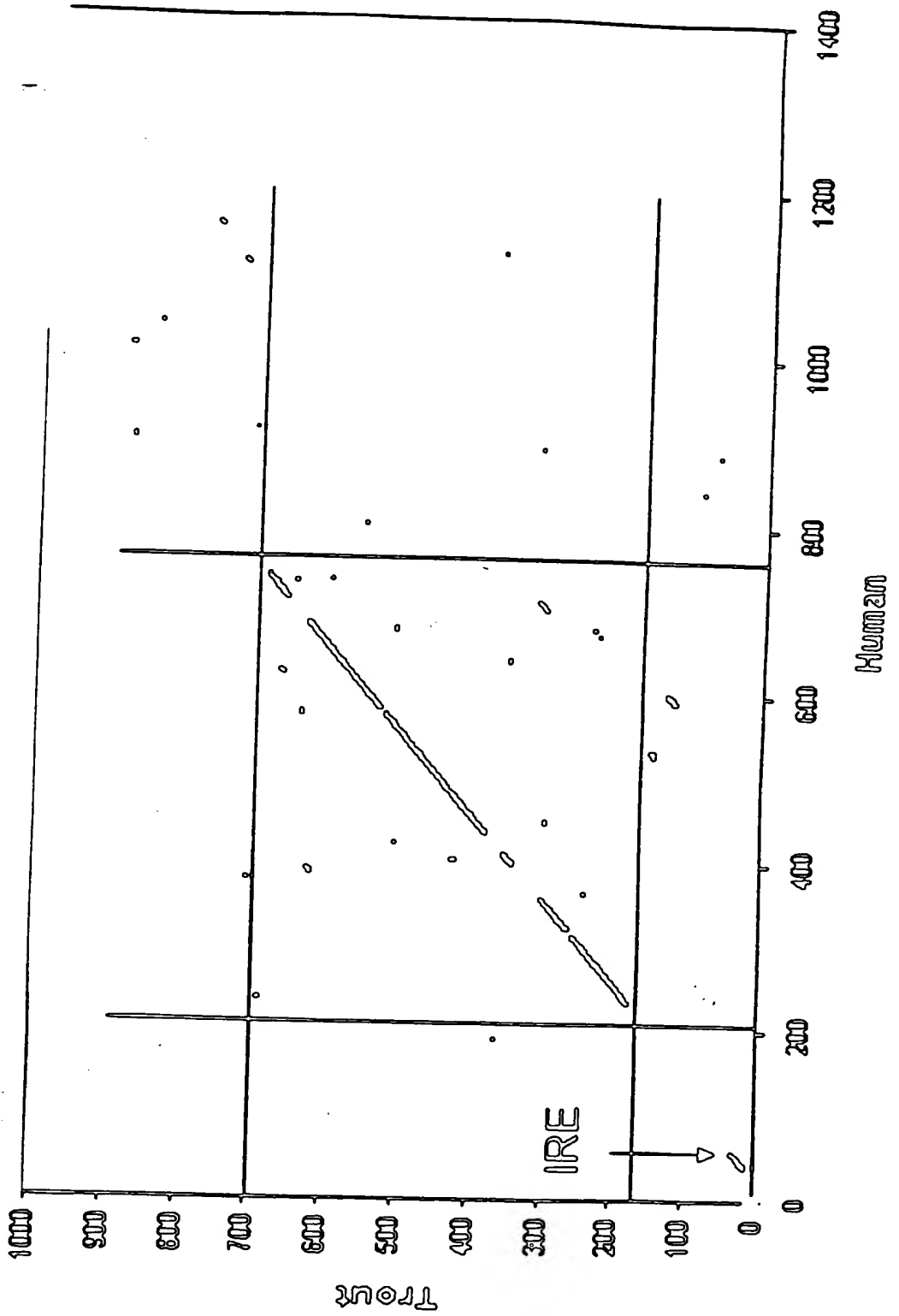


FIGURE 11

1. The first group of data points is the most common, and is found in the first group of data points.

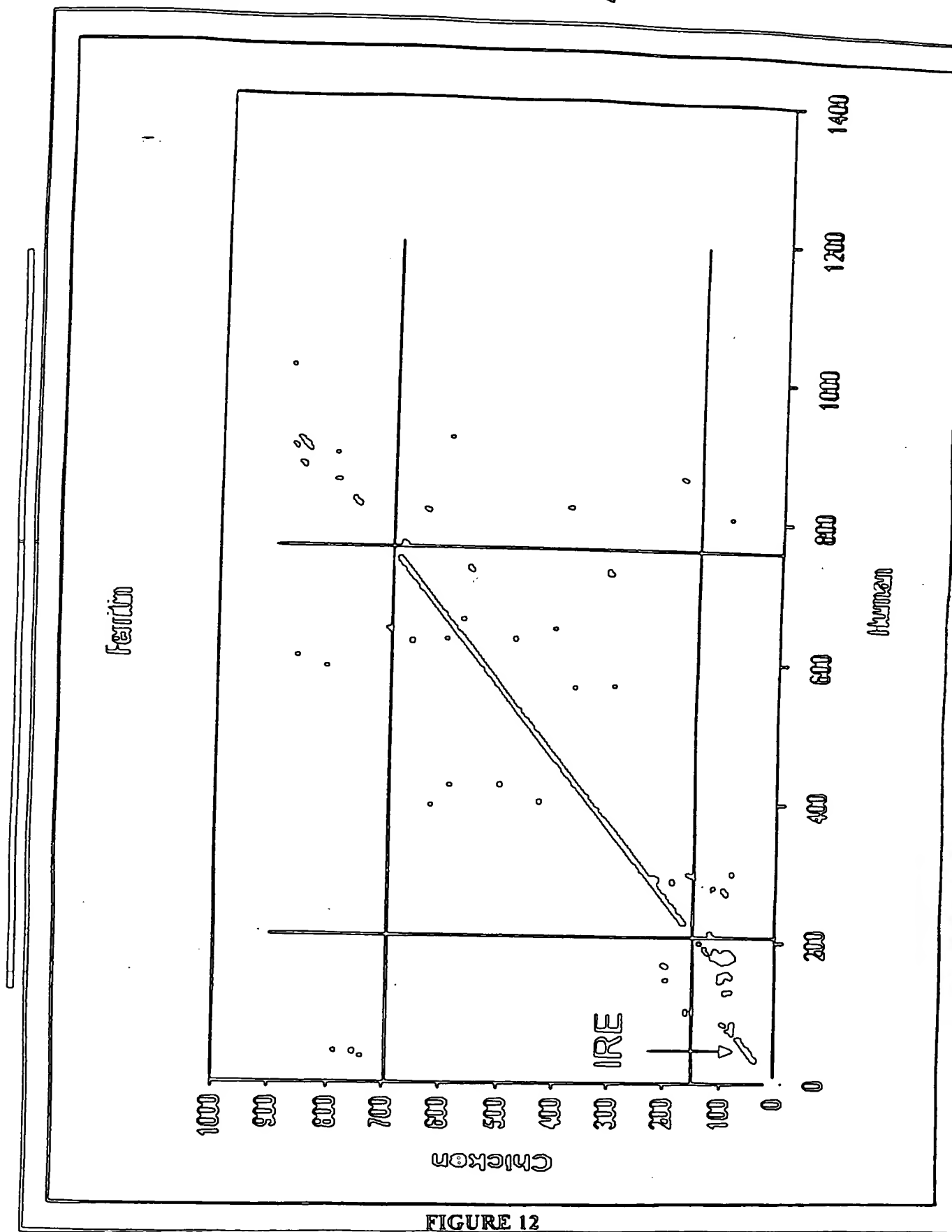
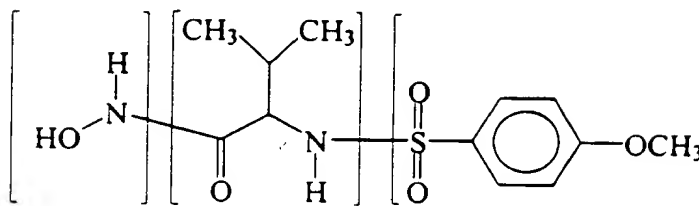
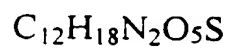
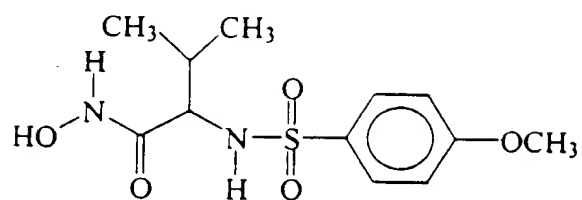


FIGURE 12



Compound CI



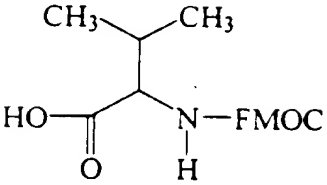
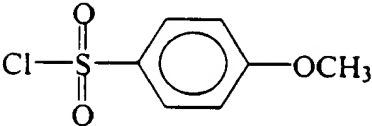
	Fi	Fii	Fiii
Molecular formula	H <sub>2</sub> NO	C <sub>5</sub> H <sub>9</sub> NO	C <sub>7</sub> H <sub>7</sub> O <sub>3</sub> S

FIGURE 14

# Addition of fragments to yield compounds

Fragment Identifier	Table			
	Structure	Name	Molecular formula	Other
F <sub>i</sub>	$\begin{array}{c} \text{H} \\   \\ \text{H}-\text{O}-\text{N}- \end{array}$	Hydroxylamine	H <sub>2</sub> NO	...
F <sub>ii</sub>	$\begin{array}{c} \text{CH}_3 \quad \text{CH}_3 \\   \quad   \\ \text{---} \text{C} \text{---} \text{C} \text{---} \text{N} \text{---} \\    \quad   \\ \text{O} \quad \text{H} \end{array}$	Amino acid	C <sub>5</sub> H <sub>9</sub> NO	...
F <sub>iii</sub>	$\begin{array}{c} \text{O} \\    \\ \text{---} \text{S} \text{---} \end{array} \text{---} \text{C}_6\text{H}_4 \text{---} \text{OCH}_3$	Sulfonyl	C <sub>7</sub> H <sub>7</sub> O <sub>3</sub> S	...

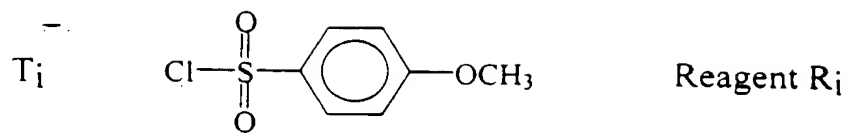
FIGURE 15

Reagents	Identifier	Name	Properties
$\text{H}-\text{O}-\text{NH}_2$ or $\textcircled{\text{P}}-\text{O}-\text{NH}_2$	R <sub>i</sub>	Hydroxylamine	...
	R <sub>ii</sub>	Fmoc blocked amino acid	...
	R <sub>iii</sub>	Sulfonylchloride	...

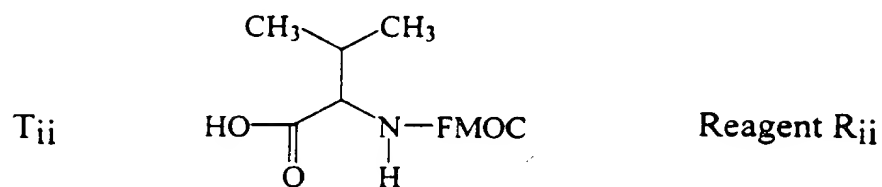
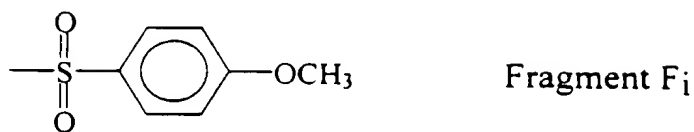
$\textcircled{\text{P}}$  = Solid support

FIGURE 16

# Transformation



↓ reaction conditions alpha



↓ reaction conditions beta



↓ reaction conditions gamma



Ⓟ = Solid support

FIGURE 17



Common Fragment / Different Reagents and Transformations

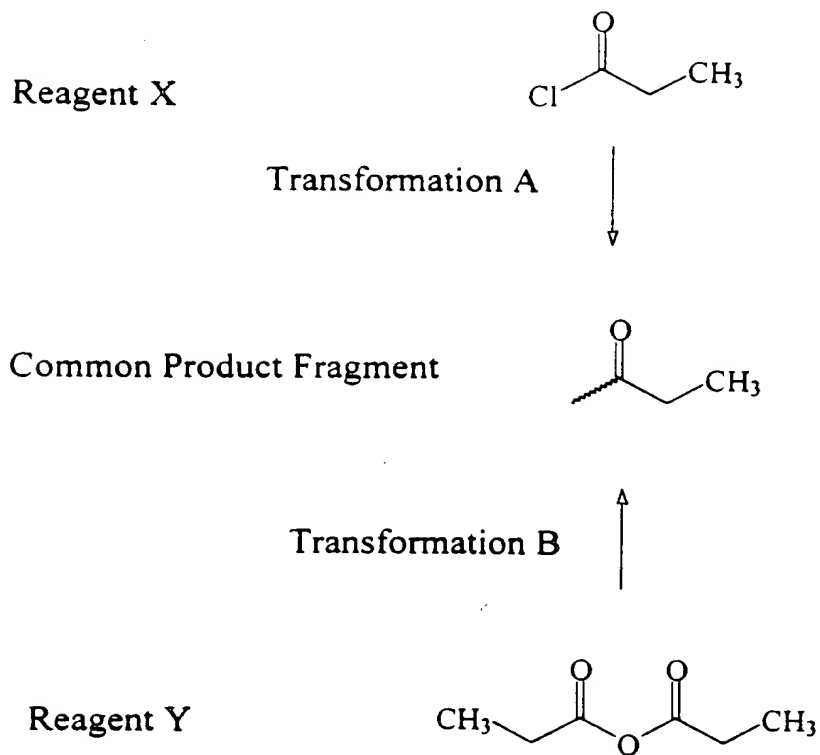


FIGURE 18

# Common Fragment / Different Reagents and Transformations

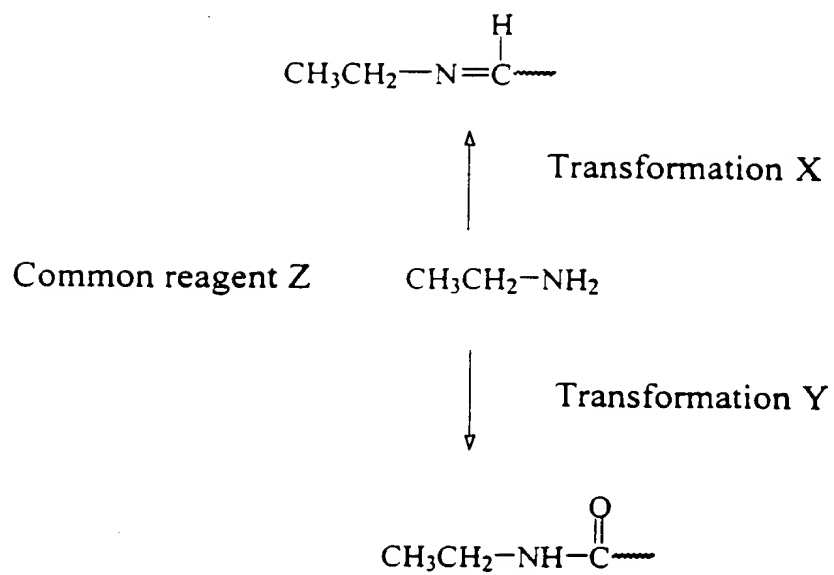


FIGURE 19A

Common Reagent

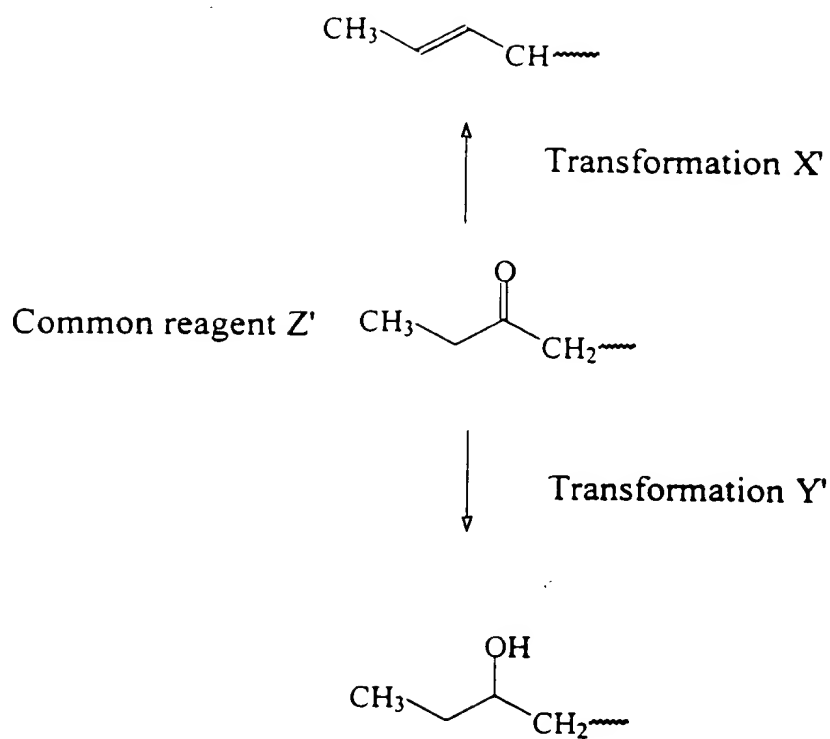
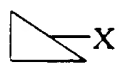


FIGURE 19B

Symbolic addition of fragments to yield compound

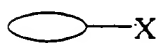
<u>Symbolic Structure</u>	<u>Symbolic Identifier</u>	<u>Molecular formula</u>
---------------------------	----------------------------	--------------------------

Fragment



$F_i'$

$C_uH_vN_w \dots$



$F_{ii}'$

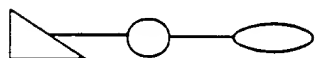
$C_uH_vN_w \dots$



$F_{iii}'$

$C_uH_vN_w \dots$

Compound



$CI'$

$C_uH_vN_w \dots$

Molecular formula  $F_i'$

+

Molecular formula  $F_{ii}'$

+

Molecular formula  $F_{iii}'$

= Molecular formula  $CI'$

FIGURE 20

# Symbolic Reagent Table

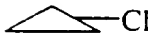
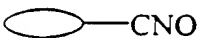
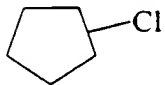
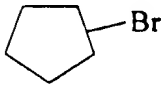
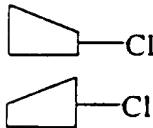
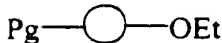

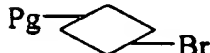
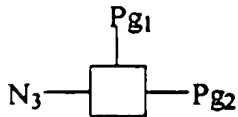
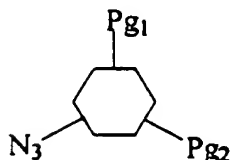
<u>Identifier</u>	<u>Name</u>	<u>Structure</u>	<u>Molecular formula</u>
R1	xxx		xxx
R2	...		...
R3	...		...
R4	...		...
R5	...		...
R6	...		...
R7	...		...
R8	...		...
R9	...		...
R10	...		...

FIGURE 21



# Symbolic Fragment Table

<u>Identifier</u>	<u>Symbolic Structure</u>	<u>Molecular formula</u>	<u>Molecular Weight</u>
F1		xxx	xxx
F2		...	...
F3		...	...
F4		...	...
F5		...	...
F6		...	...
F7		...	...
F8		...	...

FIGURE 22

# Symbolic Transformation Table

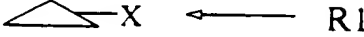
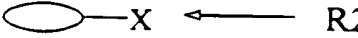
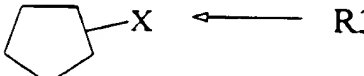
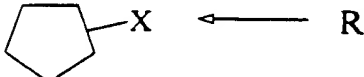
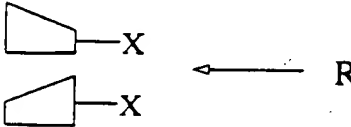

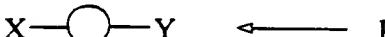

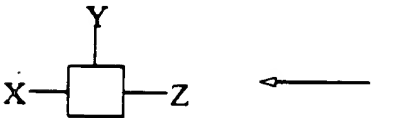
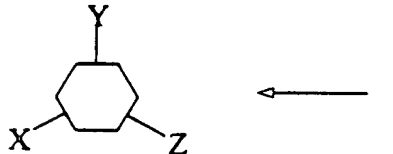
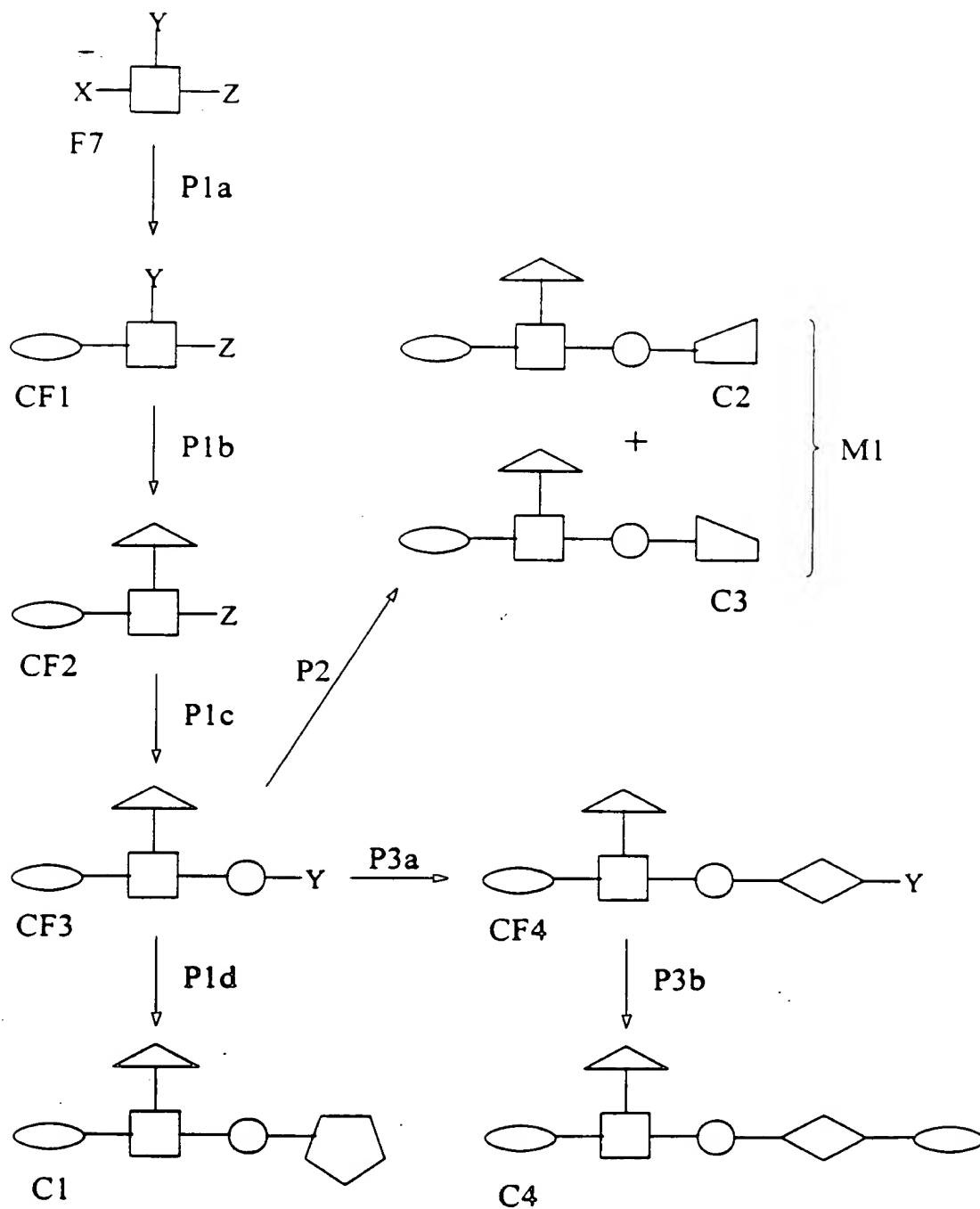
<u>Identifier</u>		<u>Symbolic Reactions</u>	<u>Reagent</u>
T1	F1	 R1	conditions $\alpha$
T2	F2	 R2	conditions $\beta$
T3	F3	 R3	conditions $\alpha$
T4	F3	 R4	conditions $\alpha$
T5	F4	 R5	conditions $\alpha$
T6	F5	 R6	conditions $\varepsilon$
T7	F5	 R7	conditions $\alpha$
T8	F6	 R8	conditions $\alpha$
T9	F7	 R9	conditions $\gamma$
T10	F8	 R10	conditions $\gamma$

FIGURE 23

# Single Compounds and Mixtures



P = synthetic path    CF = complex fragment  
 F = fragment        M = mixture  
 C = compound

FIGURE 24





Mixture 2

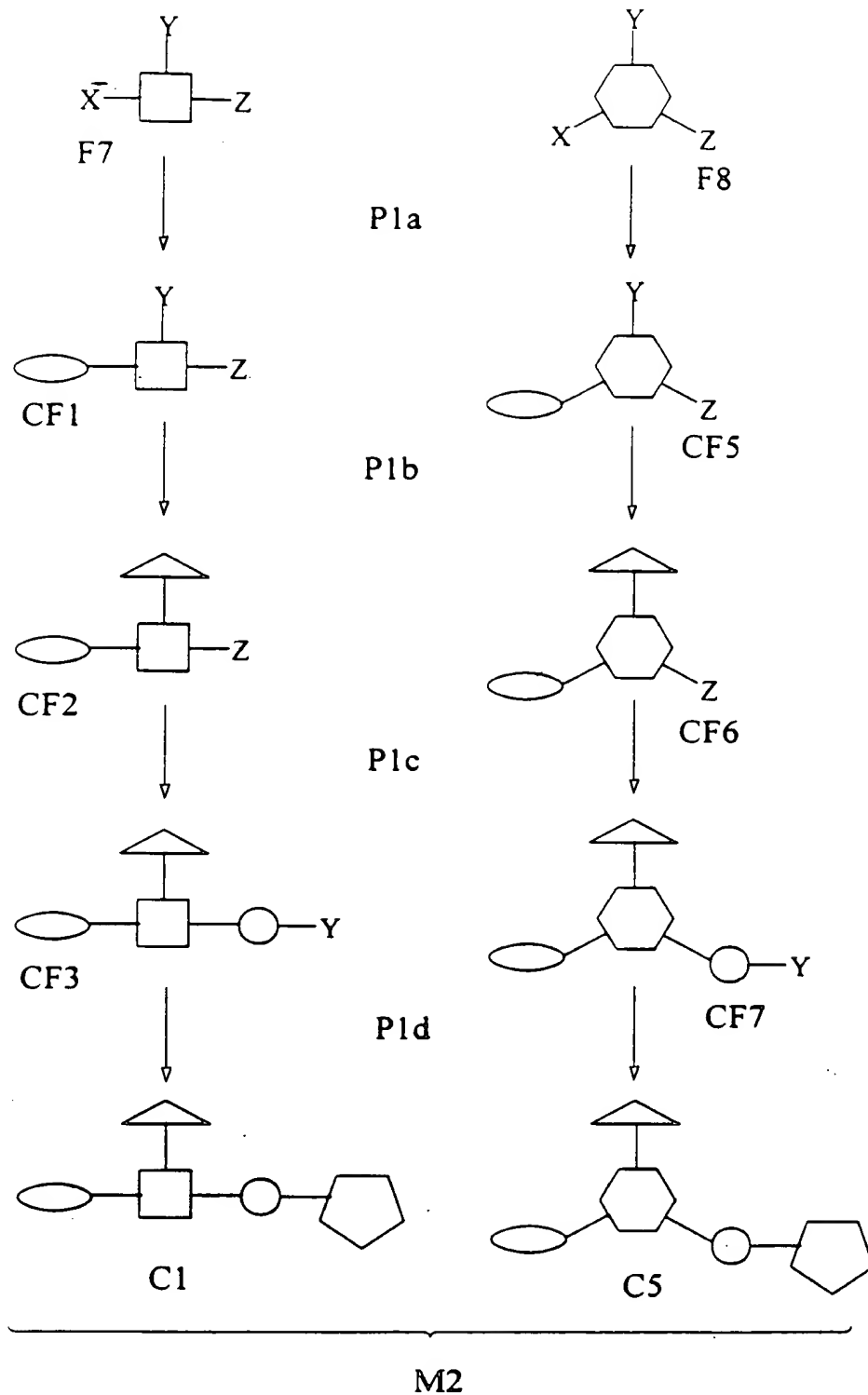


FIGURE 25

# Mixture 3

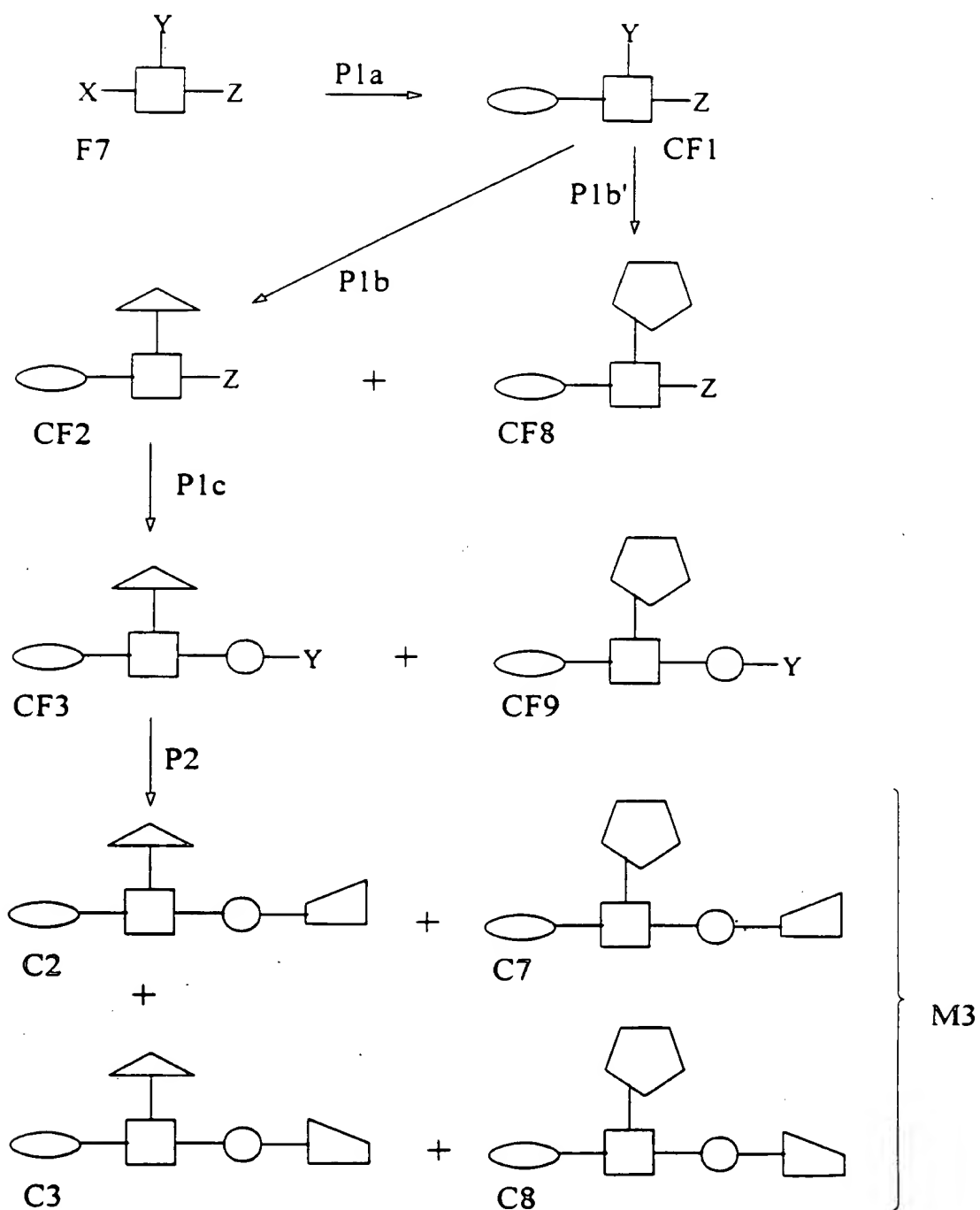
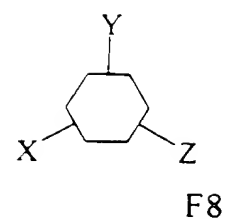
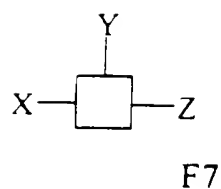
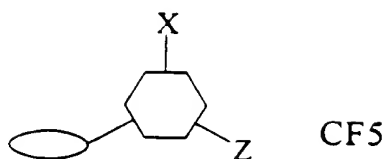
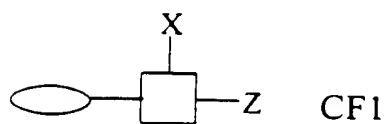


FIGURE 26

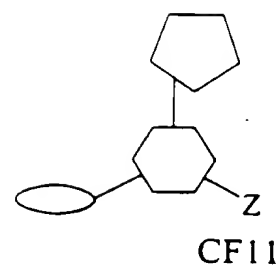
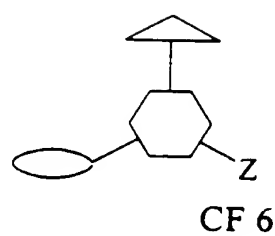
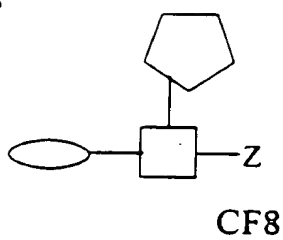
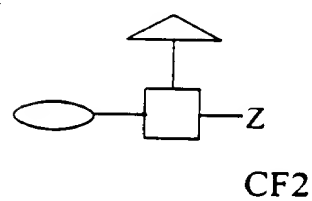
Mixture 4  
2 Starting Fragments



2 Complex Fragments



4 Complex Fragments



8 Complex Fragments

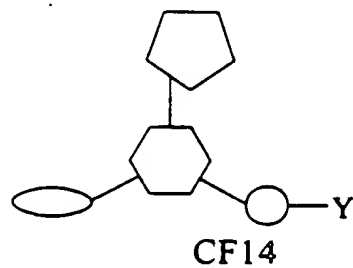
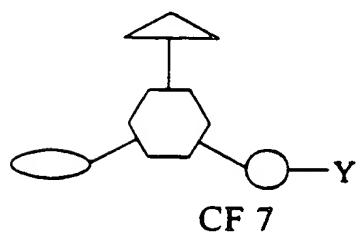
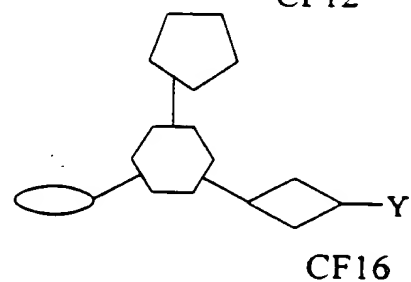
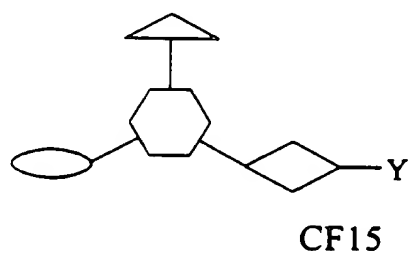
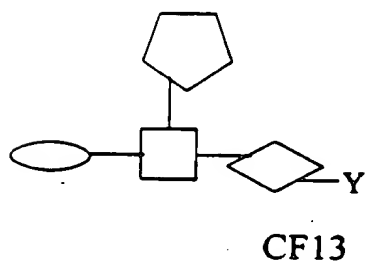
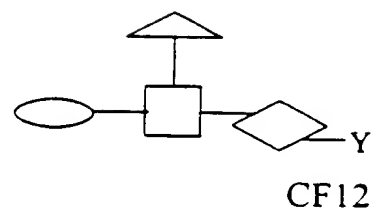
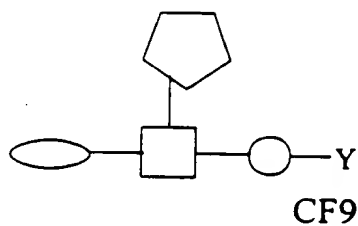
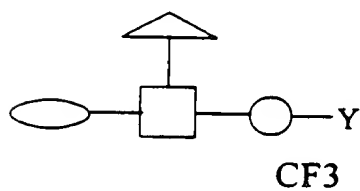


FIGURE 27A

Mixture 4 (continued)

16 compounds

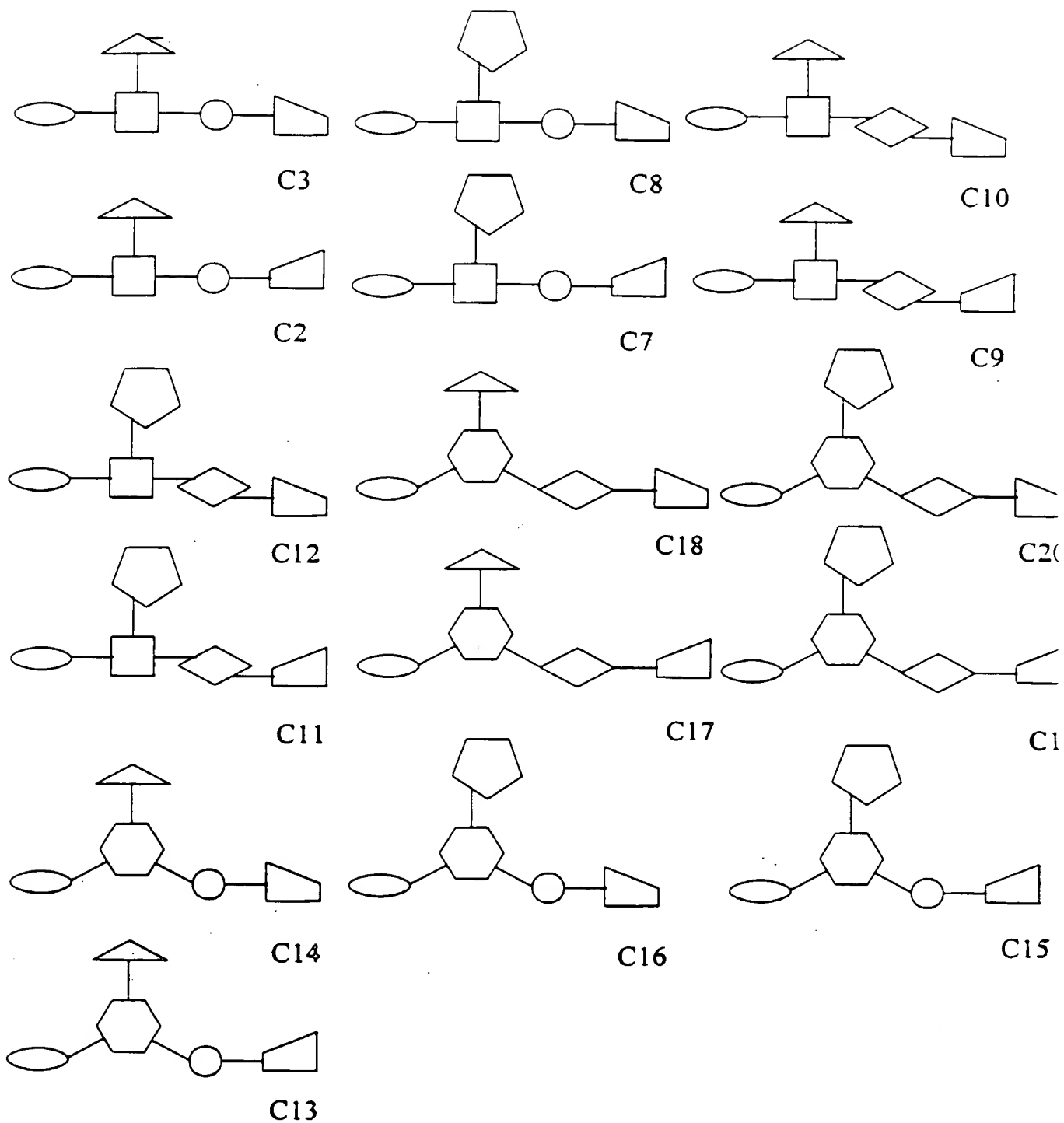


FIGURE 27B

# Tracking Table for Compound C1

## (a) By Fragments:

n	n+1	n+2
F7	F2 F1 F5	F3

## (b) By Transformations:

### Synthesis Path 1

n	n+1	n+2
T9	T2 T1 T6	T3

### Synthesis Path 2

n	n+1	n+2
T9	T2 T1 T7	T3

### Synthesis Path 3

n	n+1	n+2
T9	T2 T1 T6	T4

### Synthesis Path 4

n	n+1	n+2
T9	T2 T1 T7	T4

FIGURE 28

# Tracking Table

## Tracking M1

### Step 1

T9		
----	--	--

### Step 2

T9	T2	
----	----	--

### Step 3

T9	T2 T1	
----	----------	--

### Step 4

T9	T2 T1 T7	
----	----------------	--

### Step 5

T9	T2 T1 T7	T5 <sup>1</sup>
----	----------------	-----------------

C2

### Step 5

T9	T2 T1 T7	T5 <sup>2</sup>
----	----------------	-----------------

C3

FIGURE 29



Tracking M2

Step 1

n	n+1	n+2
T9		

Step 1

n	n+1	n+2
T10		

Step 2

n	n+1	n+2
T9	T2	

Step 2

n	n+1	n+2
T10	T2	

Step 3

n	n+1	n+2
T9	T2 T1	

Step 3

n	n+1	n+2
T10	T2 T1	

Step 4

n	n+1	n+2
T9	T2 T1 T7	

Step 4

n	n+1	n+2
T10	T2 T1 T7	

Step 5

n	n+1	n+2
T9	T2 T1 T7	T4

Step 5

n	n+1	n+2
T10	T2 T1 T7	T4

C1

C5

FIGURE 30

# Tracking Table

## Tracking M3

Step 1

T9		

Step 2

T9	T2	

Step 3

T9	T2 T1	

Step 3

T9	T2 T3	

Step 4

T9	T2 T1 T7	

Step 4

T9	T2 T3 T7	

Step 5

T9	T2 T1 T7	

Step 5

T9	T2 T1 T7	T5 <sup>2</sup>

Step 5

T9	T2 T3 T7	T5 <sup>1</sup>

Step 5

T9	T2 T3 T7	T5 <sup>2</sup>

C2

C3

C7

C8

FIGURE 31



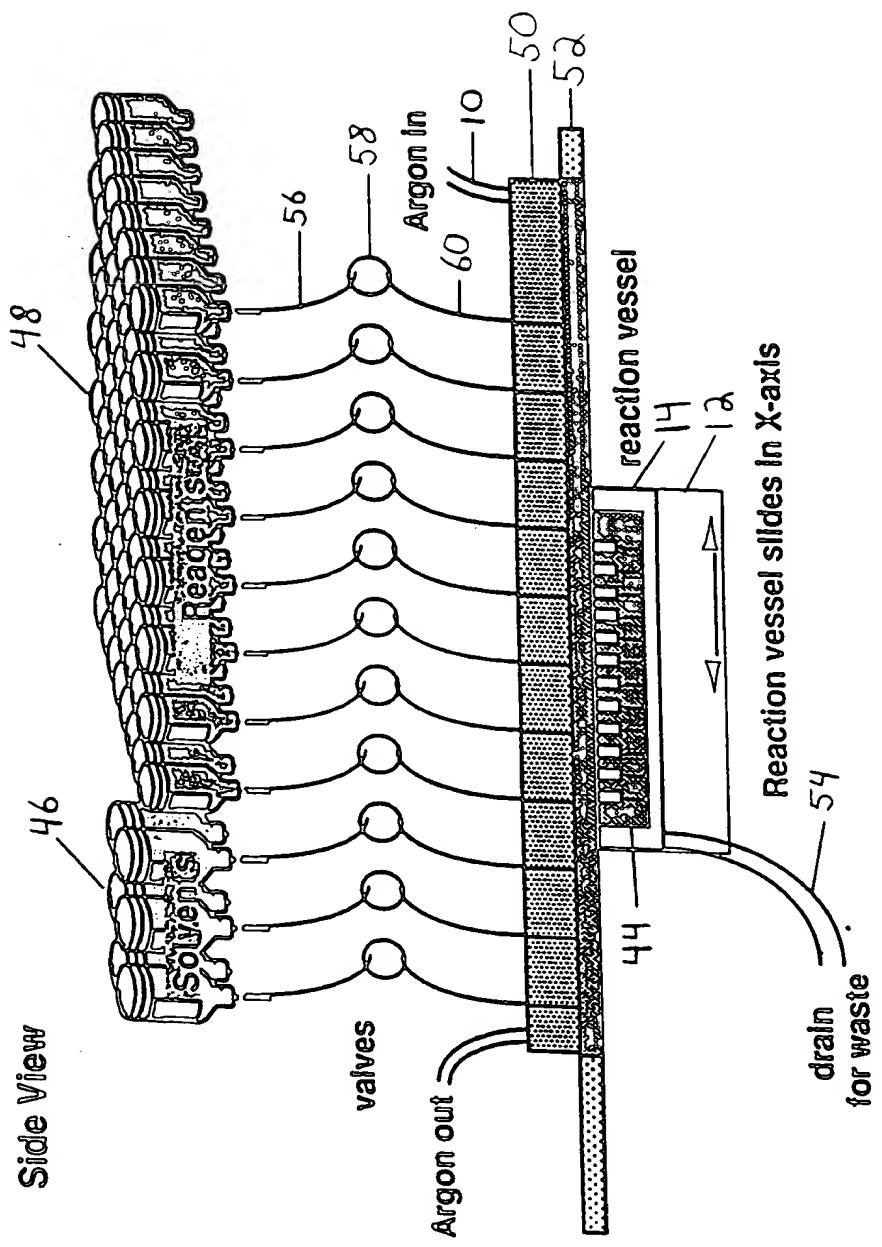


FIGURE 32

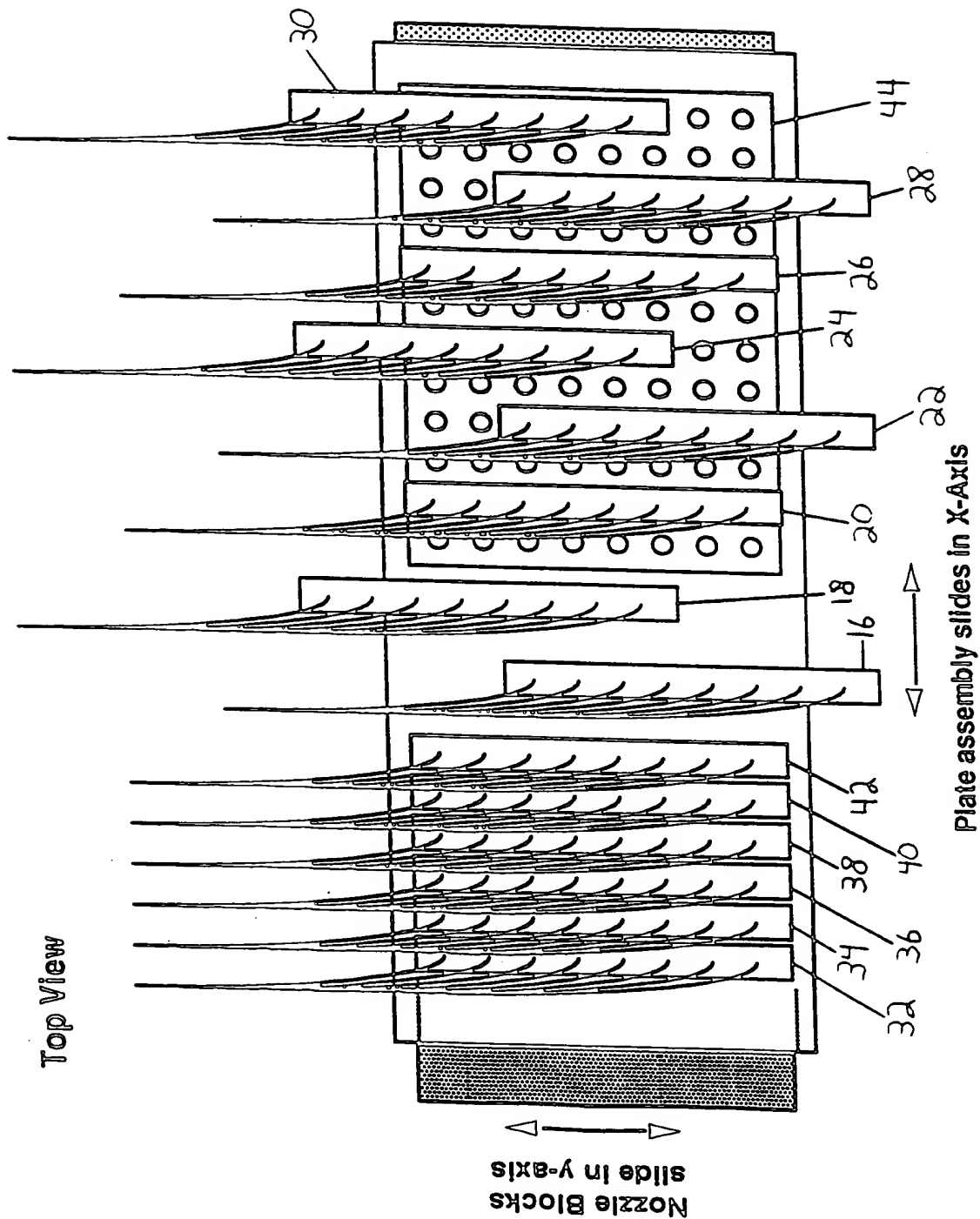


FIGURE 33

# Synthesis of hydroxamic acids from alcohol resin

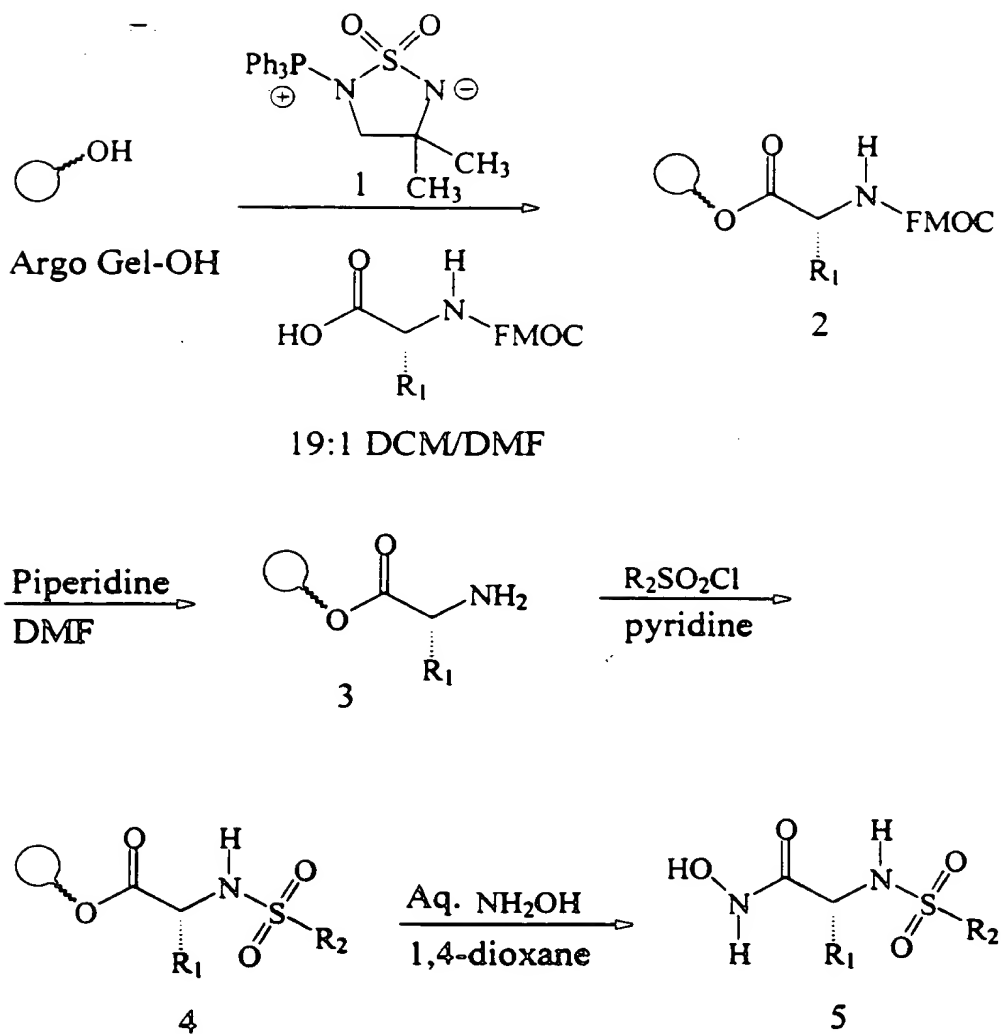


FIGURE 34

# Synthesis of hydroxamic acids from hydroxylamine resin

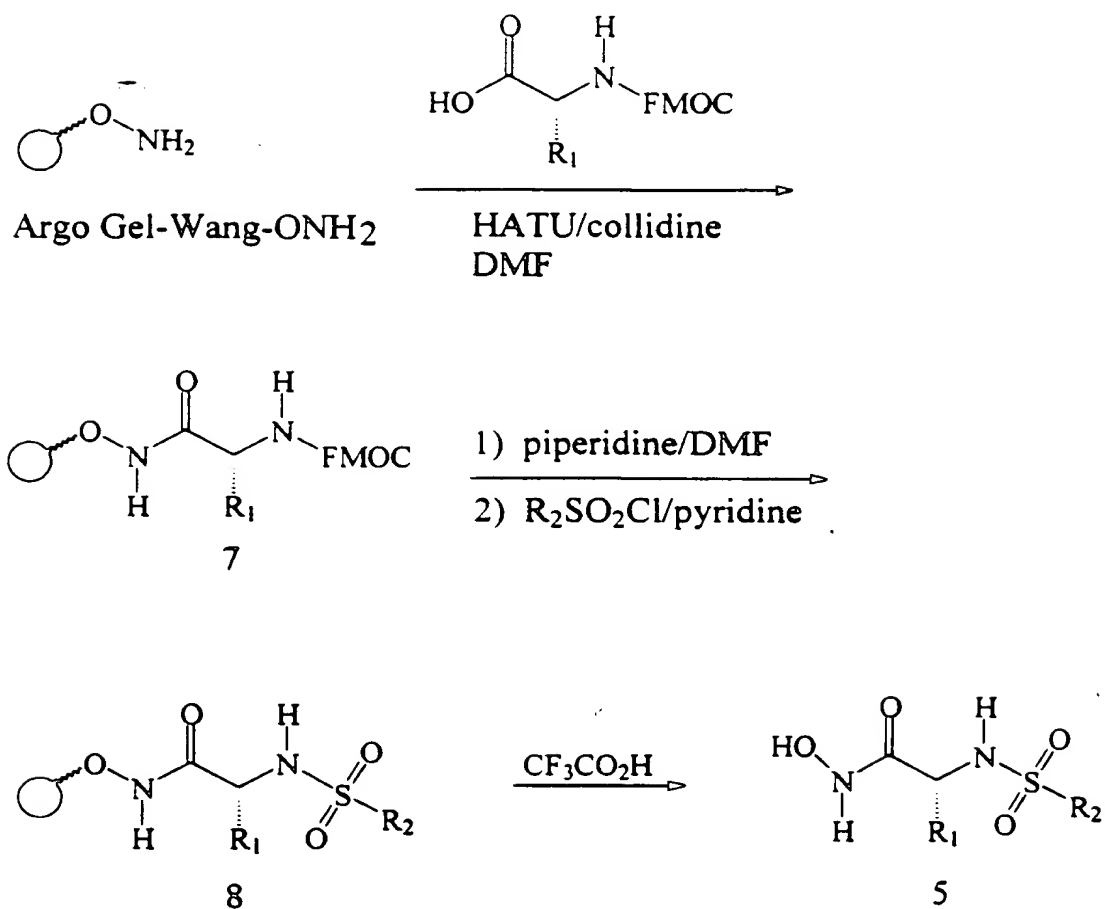


FIGURE 35

A diagram of a ribonucleoprotein complex. On the left, a 5' end is labeled. Below it, a sequence of nucleotides is shown: G-G-A-C-G-C on the top strand and C-C-U-G-C-G on the bottom strand. To the right, a larger RNA structure is depicted with a sequence of U-A-C-U-C-U-G-U-U-A-C-G-A-G-G-U-U on the top strand and C-A-G-U-A-G-A-C-G-G-A-A-C-C-G-C on the bottom strand. Several large, dark, triangular shapes representing protein subunits are attached to the RNA. Two of these subunits are labeled 'B' and 'C'.

•

# Biological Activity and Binding Energy for Structures Docked to TAR with Solvation/Desolvation Energy

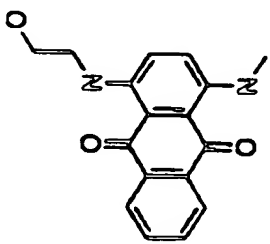
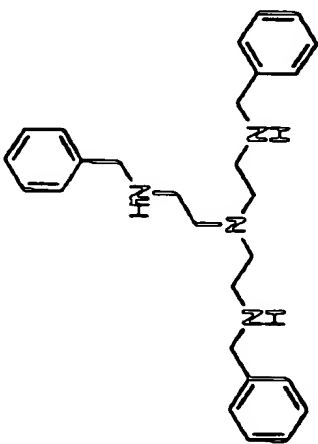
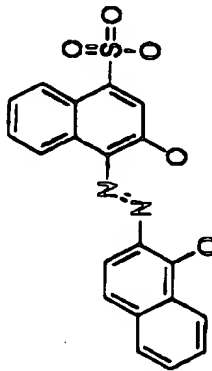
ACD Code	Structure	Calc. $\Delta G$ of binding (kcal/mole)	IC <sub>50</sub> ( $\mu$ M)
00001199		-5.1	<2
00192509		-8.5	<2
00003934		-5.1	<50

FIGURE 37

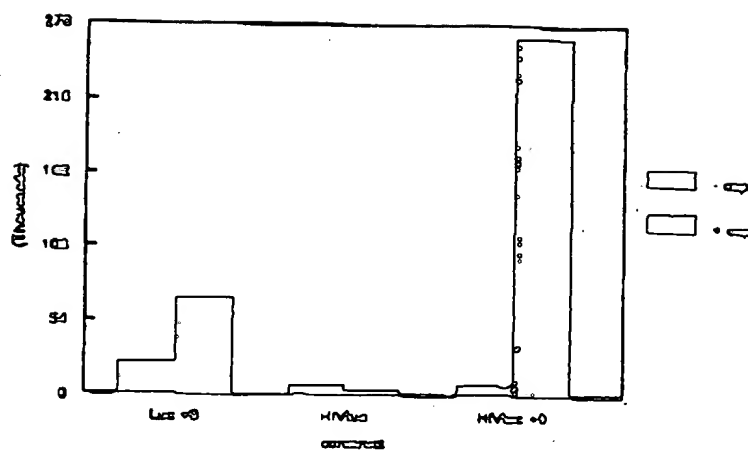


FIGURE 38A

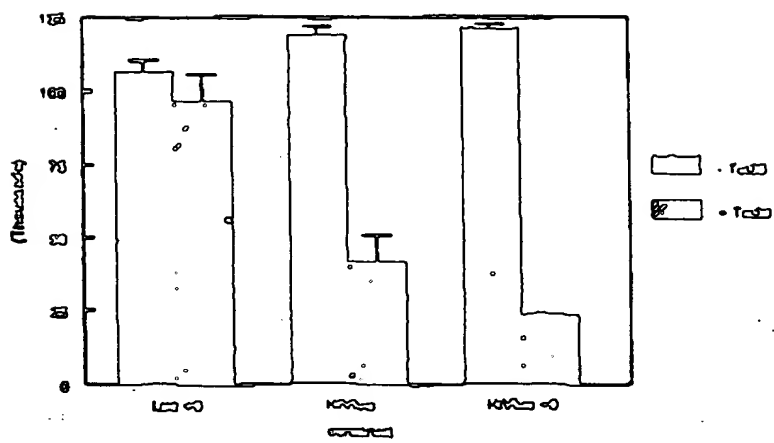


FIGURE 38B

# Inhibition of translation by DeepBlue-3 in WGL

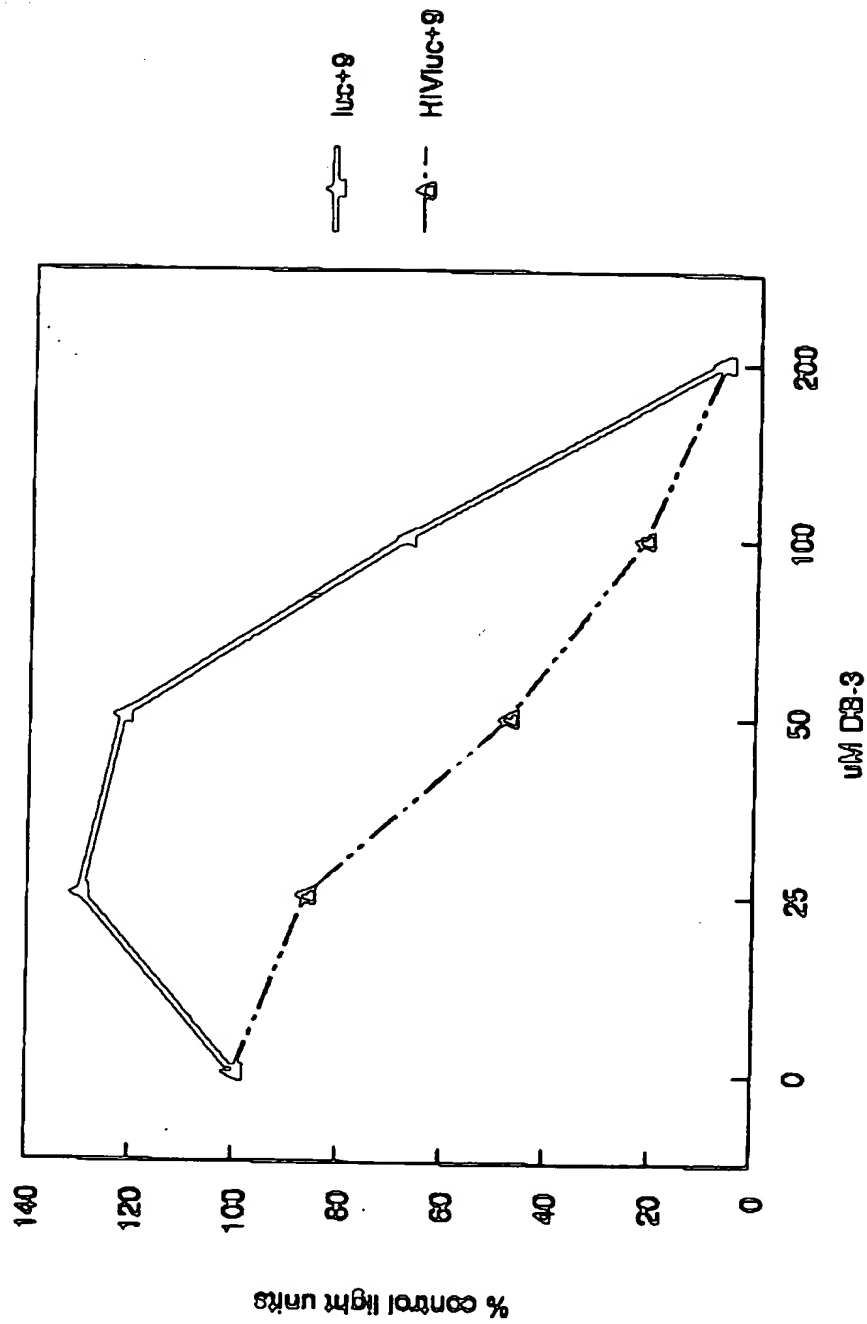


FIGURE 39



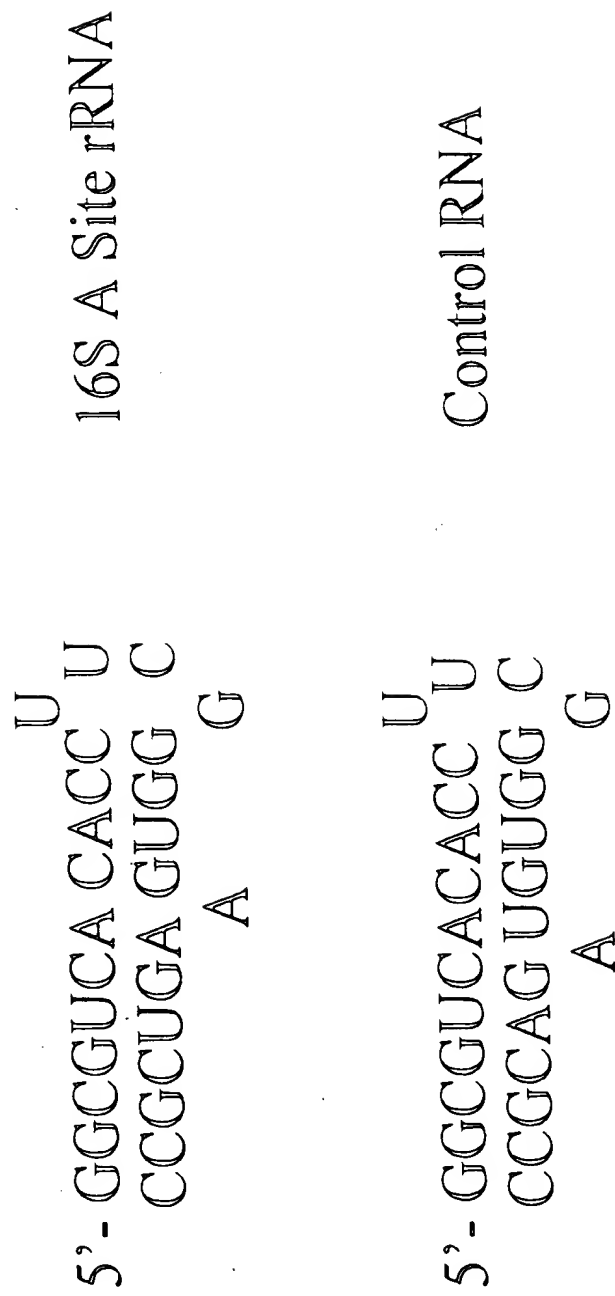
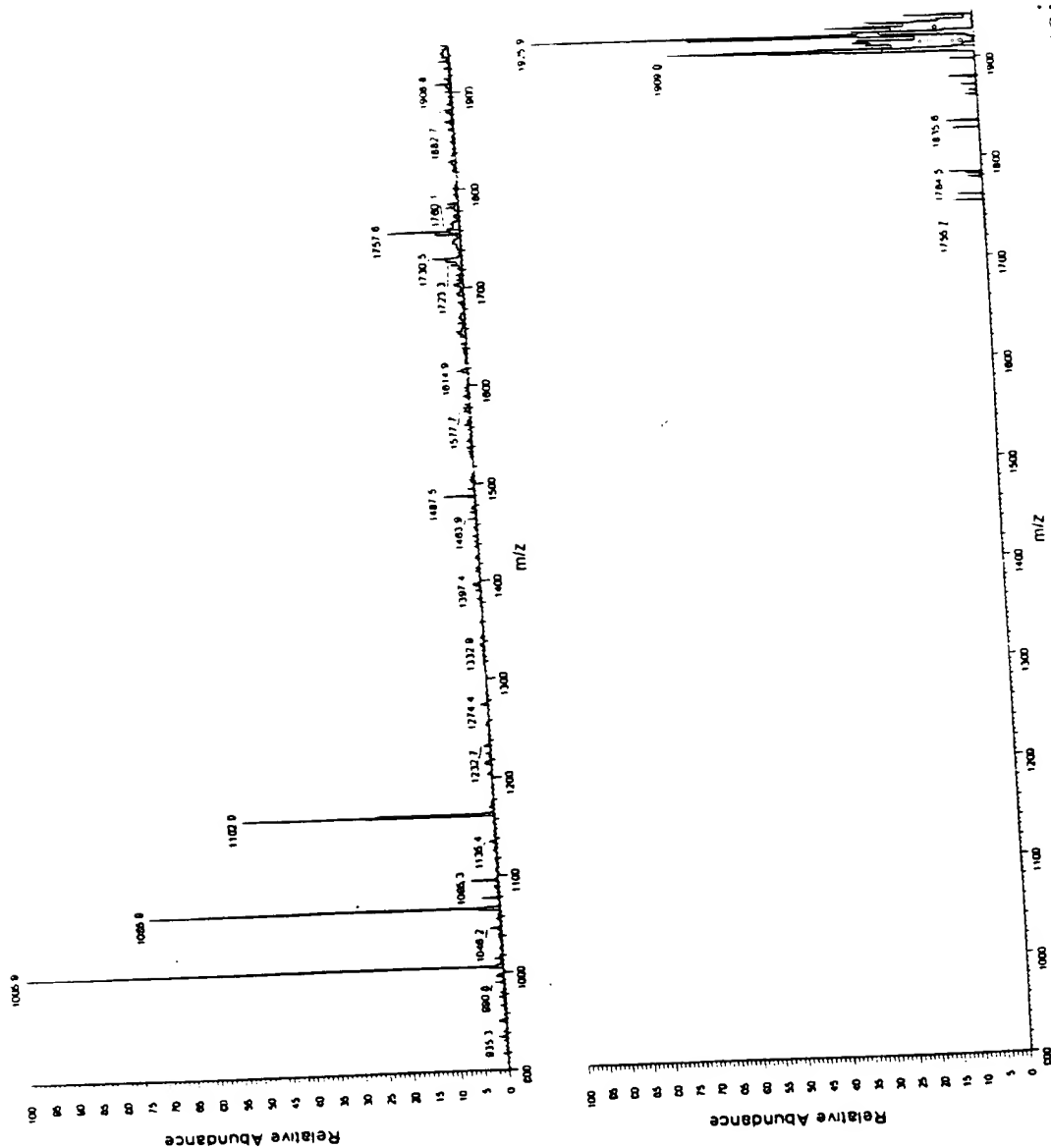
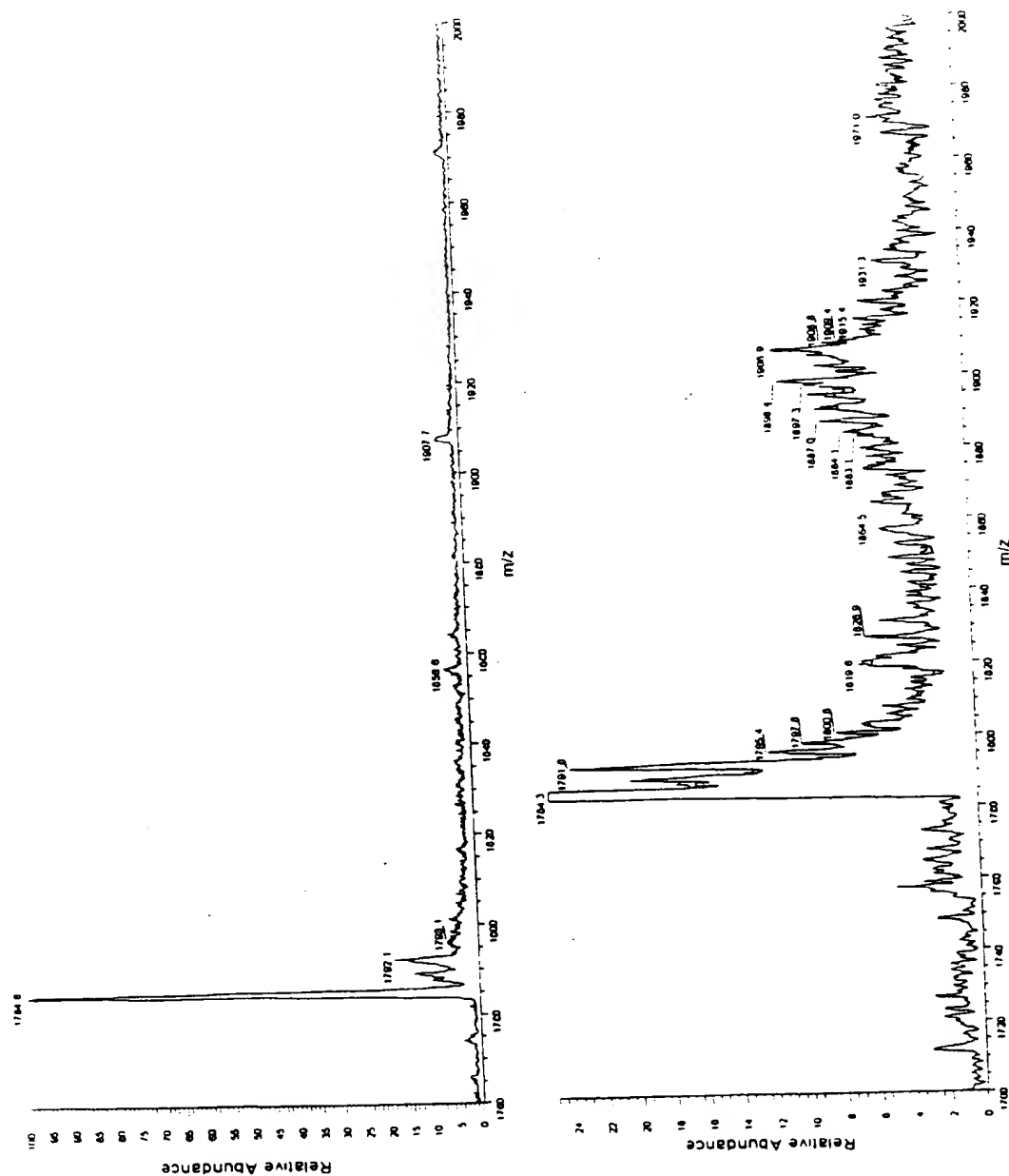


FIGURE 40 Sequence and structure of 27mer RNA target



MS/MS of control RNA/DNA (upper); control+paromomycin (lower)

FIGURE 41

[illegible]

RNA/DNA chimera+paramomycin (upper); chimera+library (lower)

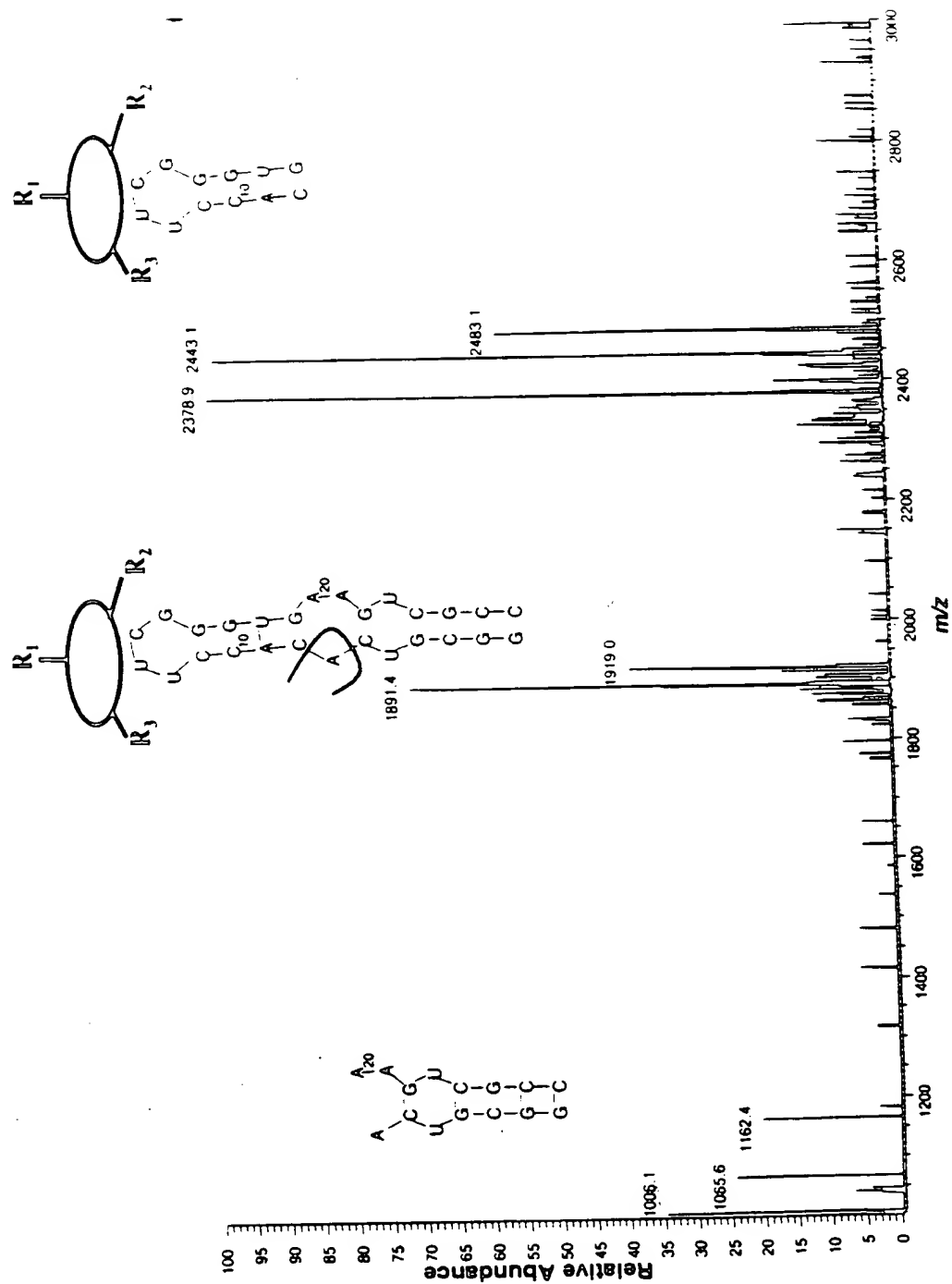
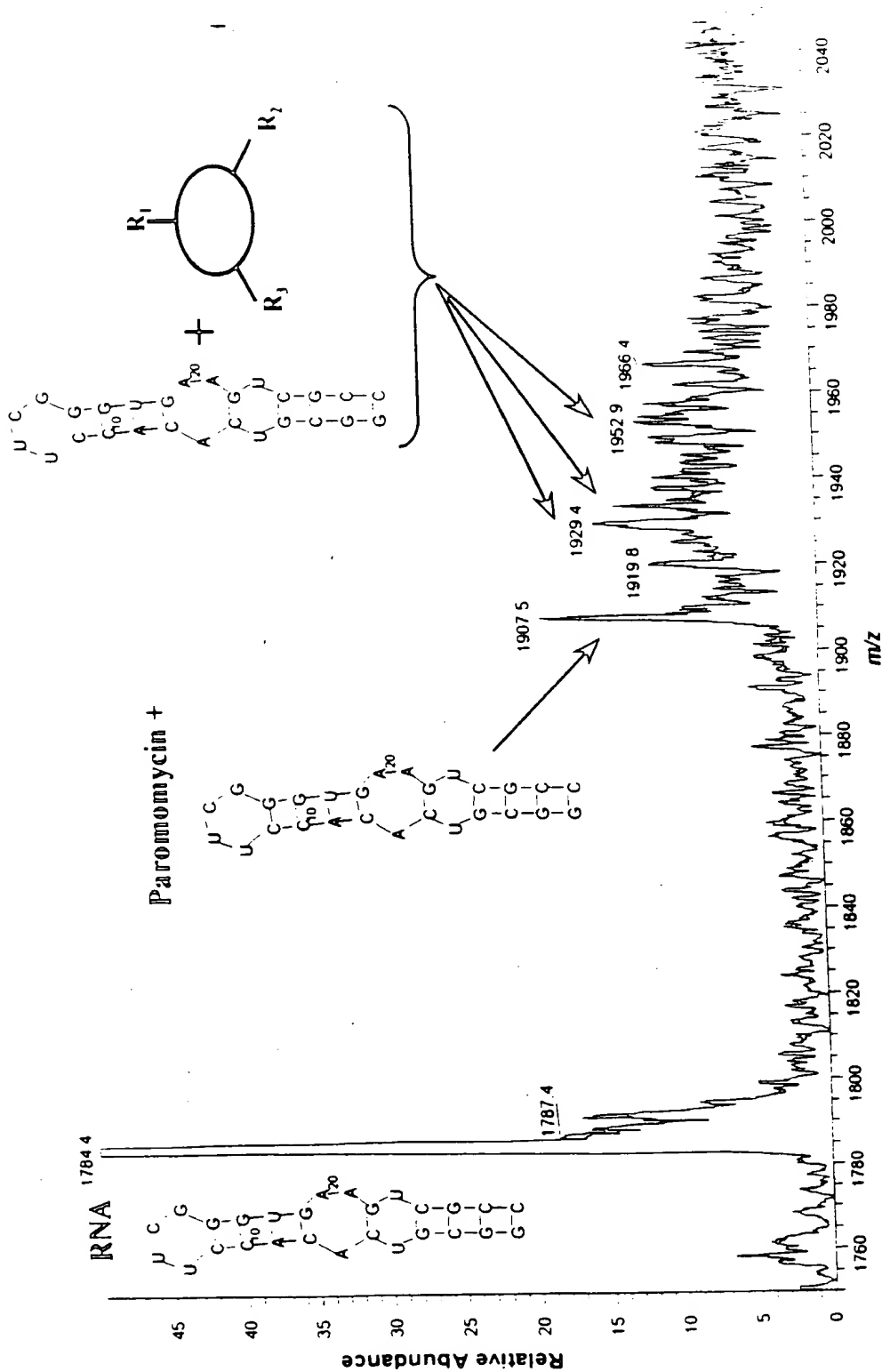
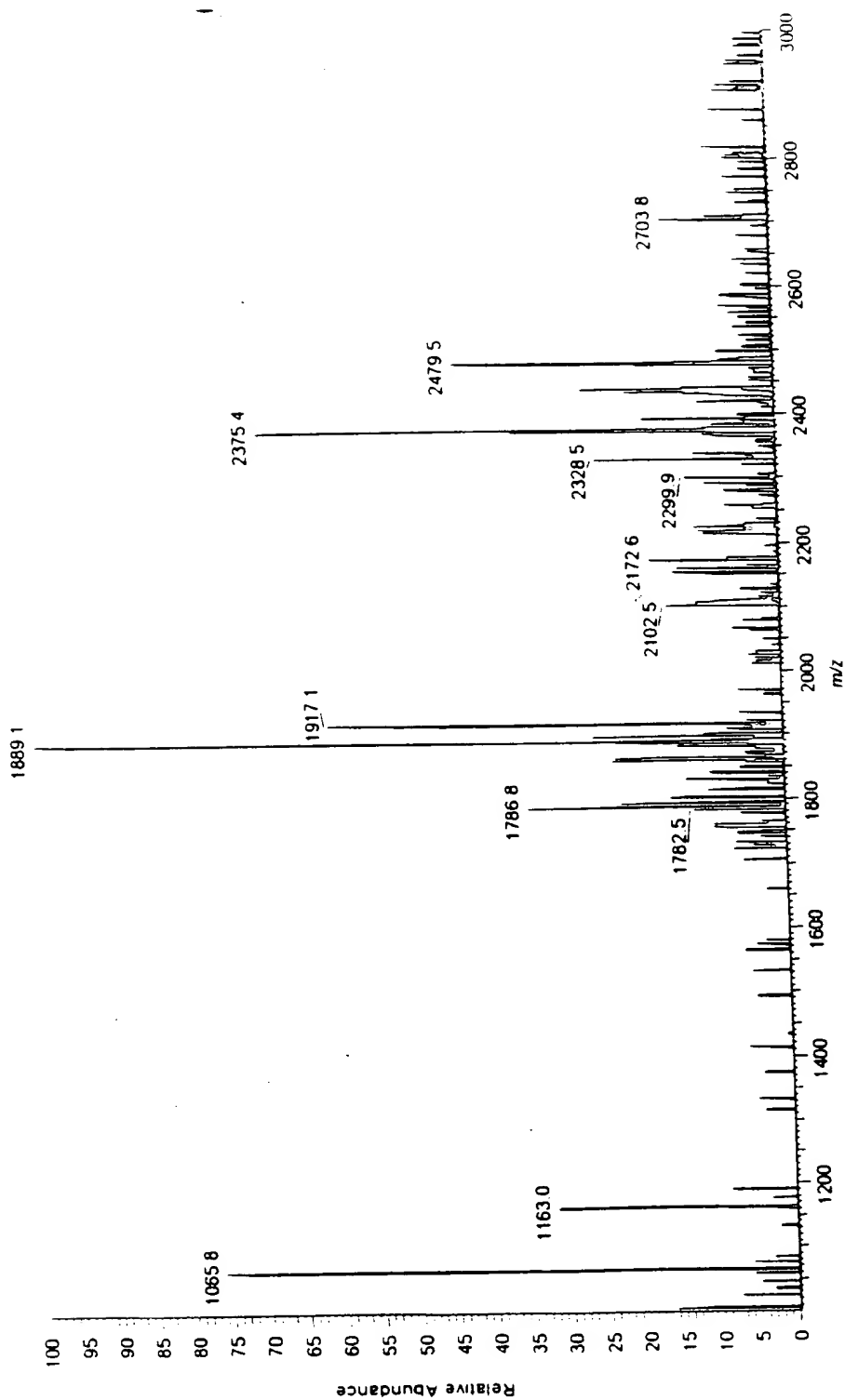


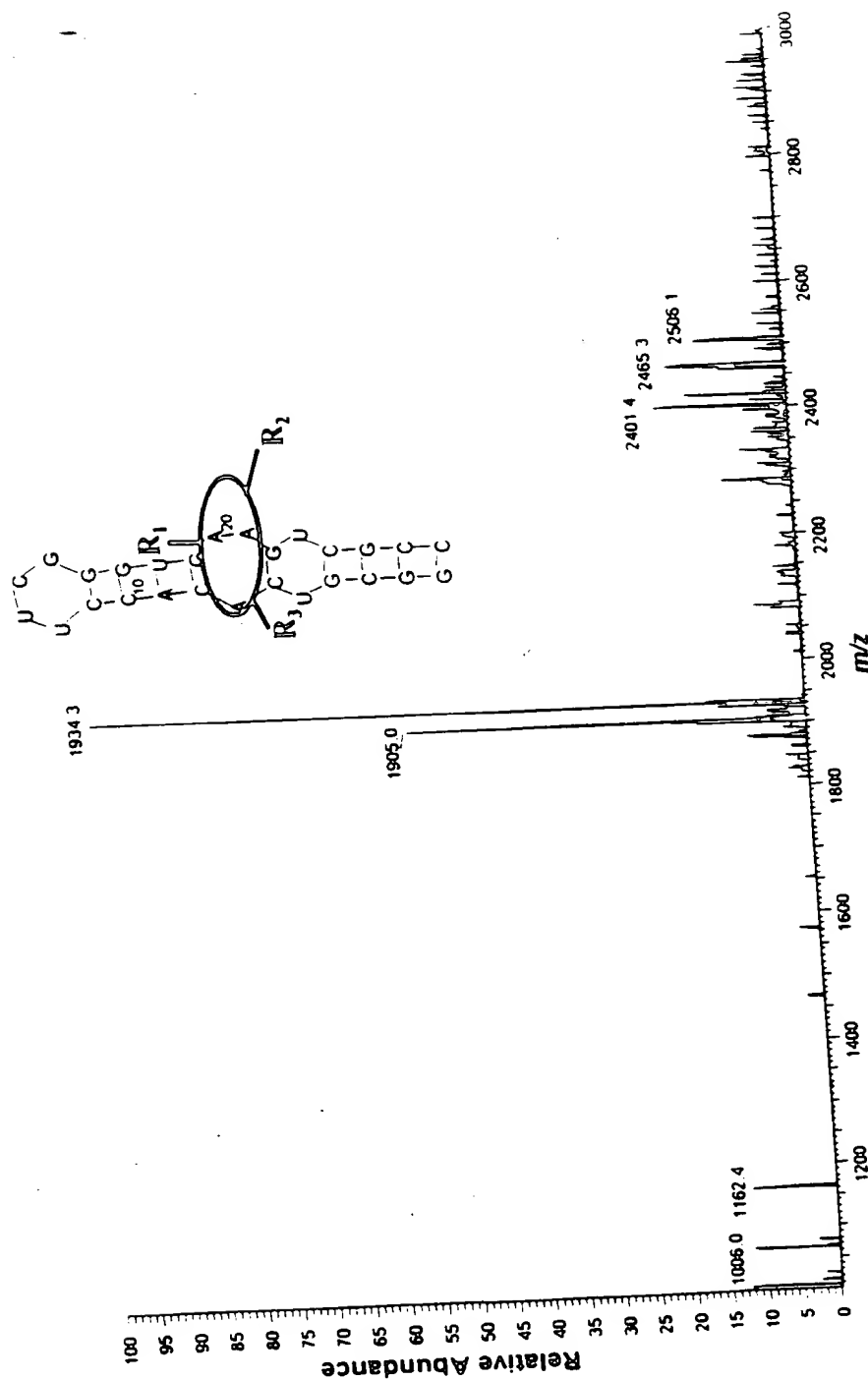
FIGURE 43 MS-MS analysis of member bound to RNA/DNA chimera



**FIGURE 44**  
**ESI-MS of RNA/DNA chimera bound to paromomycin and library**



**FIGURE 45** MS/MS of RNA/DNA chimera + compound with mass 665.1 not bound at the A-site



**MS-MS analysis of member bound to RNA/DNA chimera at the A-Site**





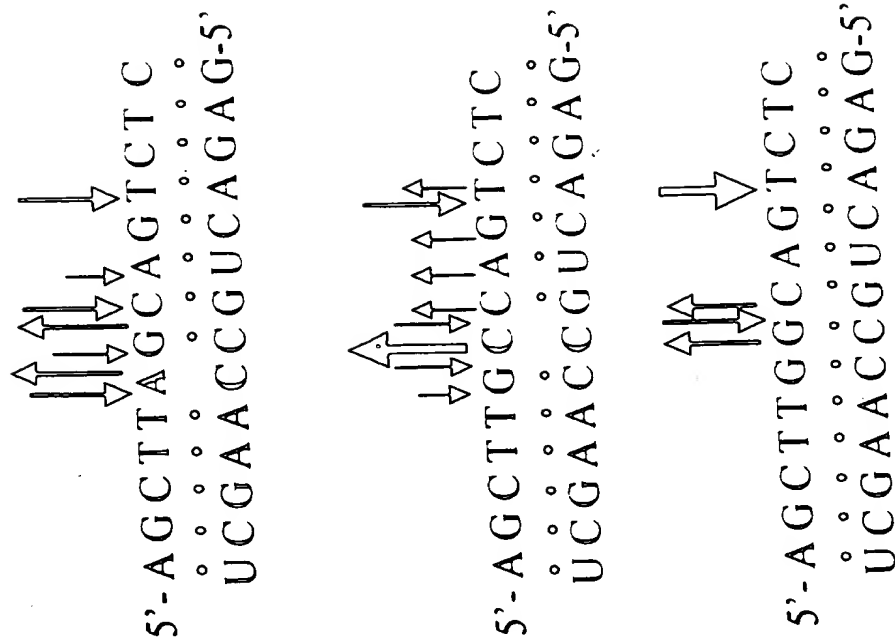
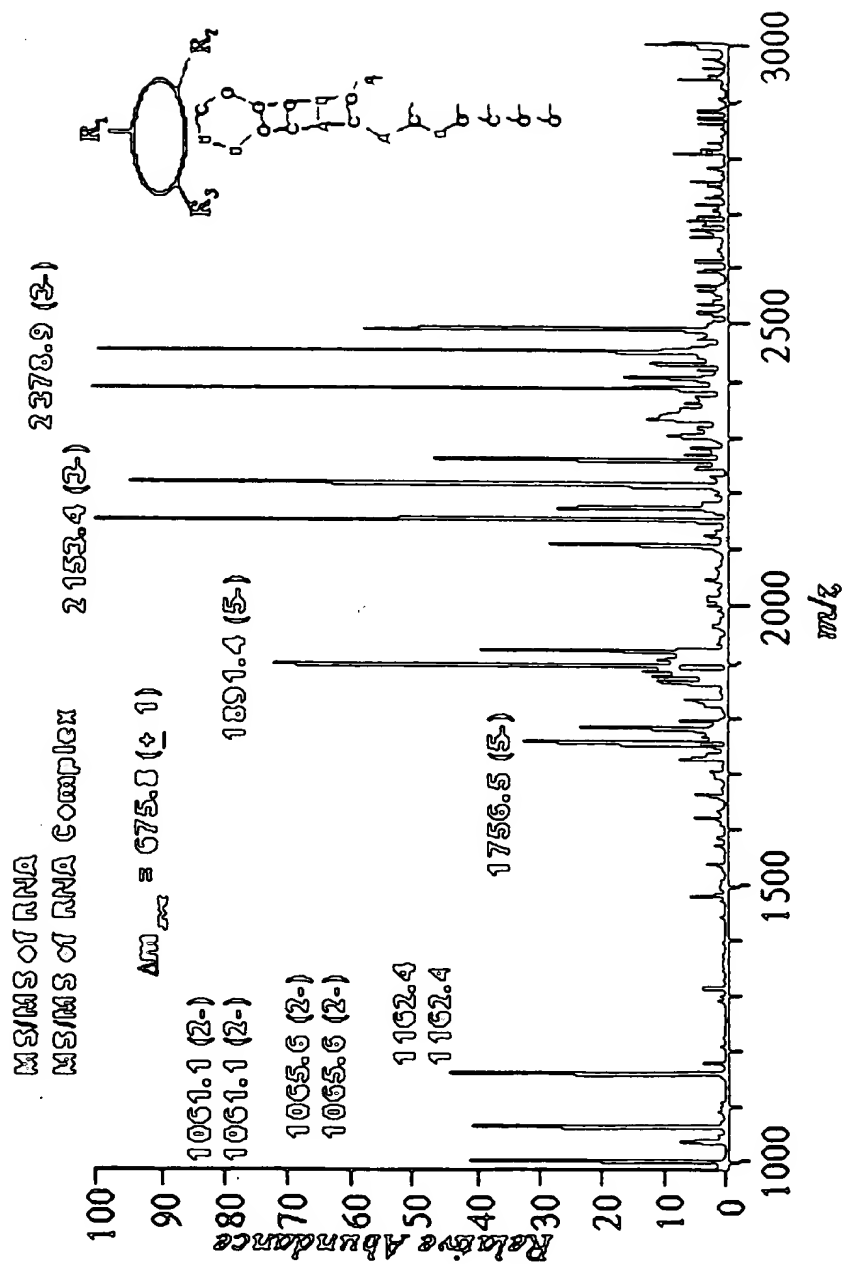
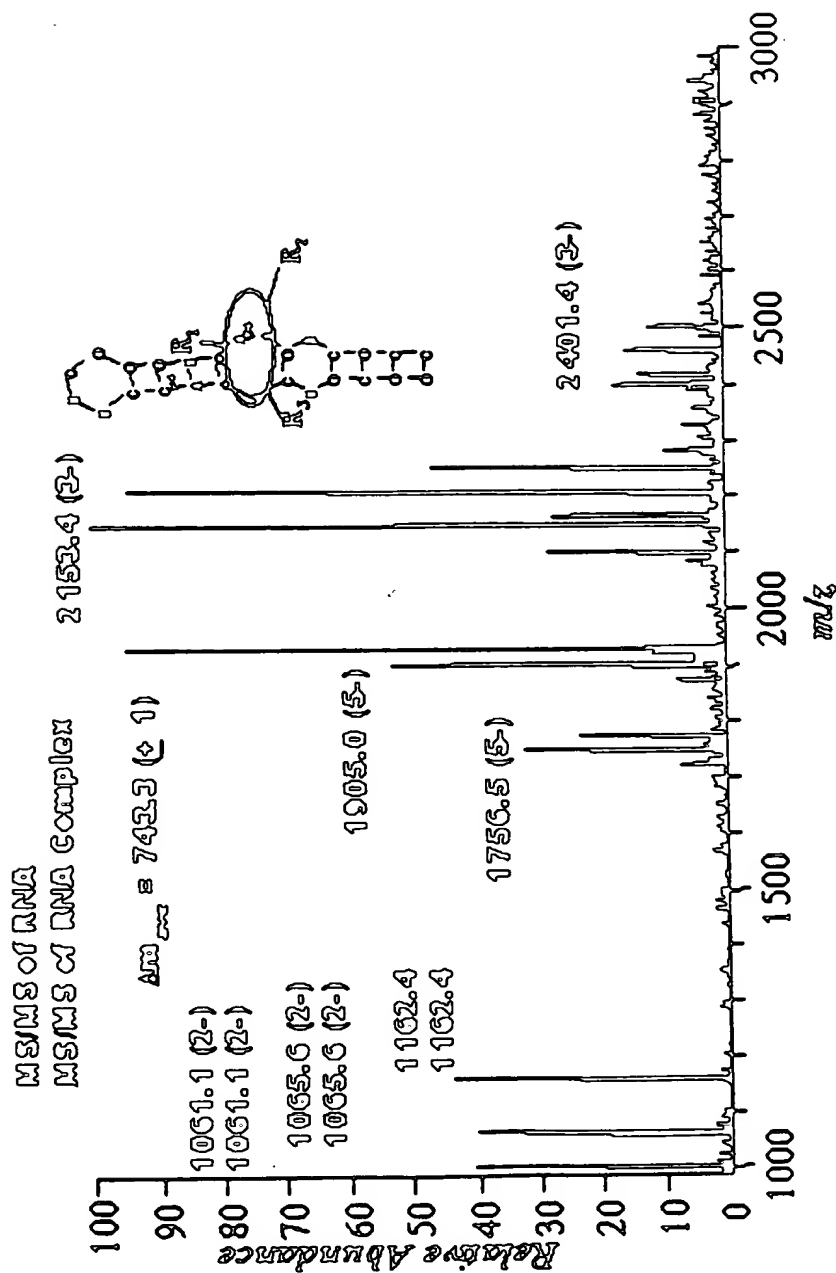


FIGURE 48 MS Fragmentation of DNA:RNA duplexes



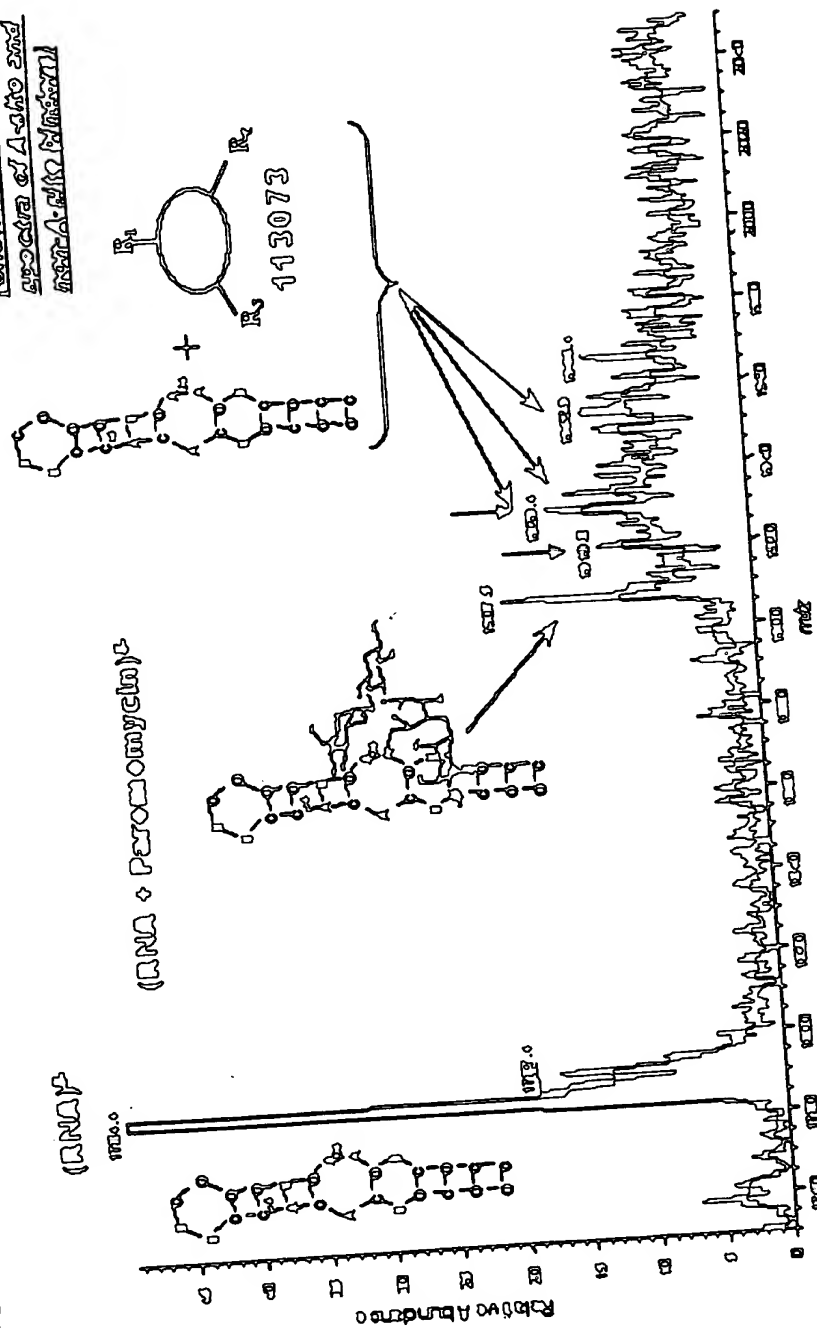
# MASS ANALYSIS OF BINDING LOCATION non-A site binder

FIGURE 50



MASS analysis of 16S A site RNA plus  
216 member library  
(performed on quadrupole ion trap)

FIGURE 51



# High Precision ESI-FT/ICR Mass Measurement of 16S A site RNA/Paromomycin Complex

Use of unbound RNA as internal mass standard provides low ppm mass measurement errors

FIGURE 52

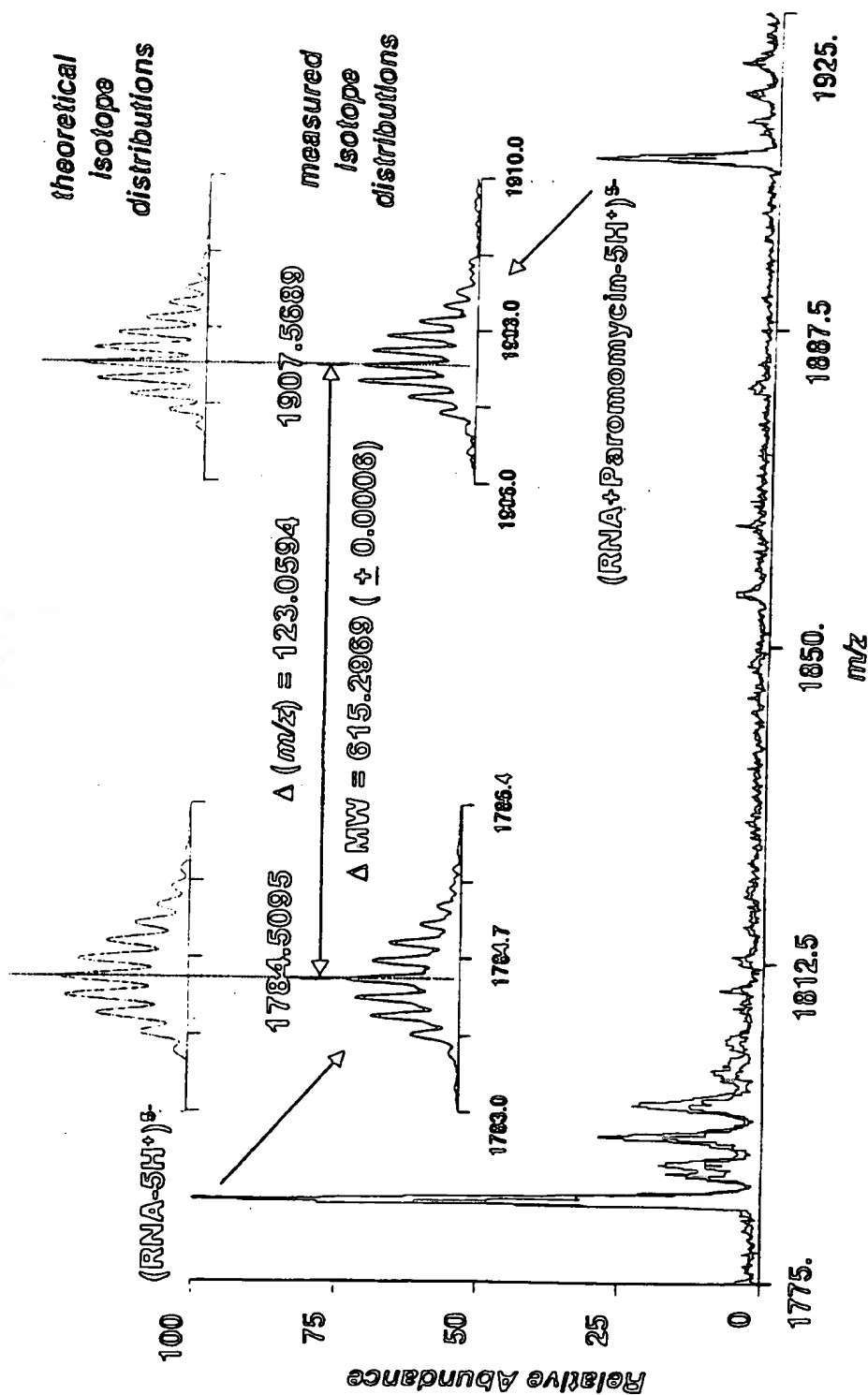


Figure 53

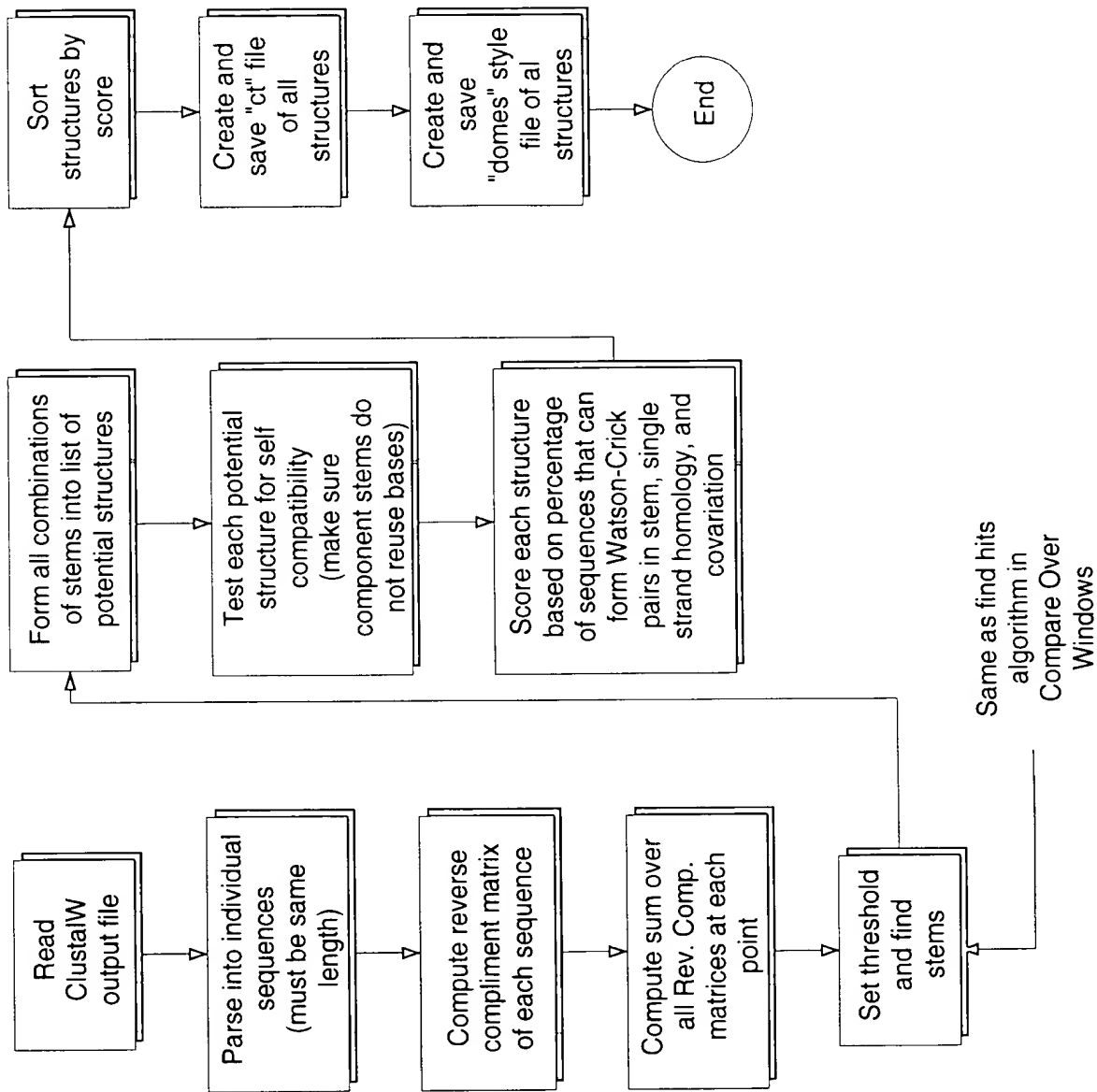
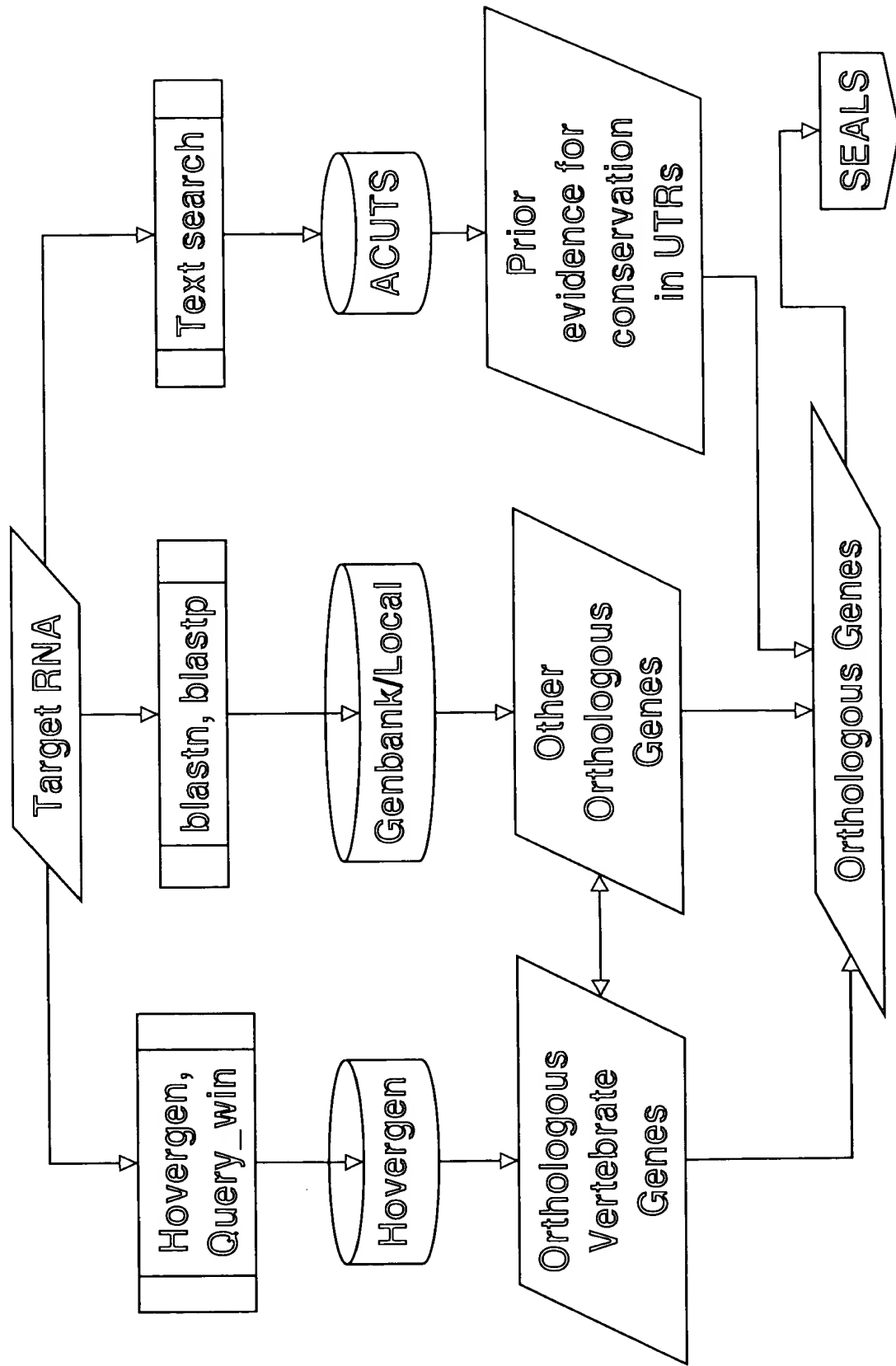
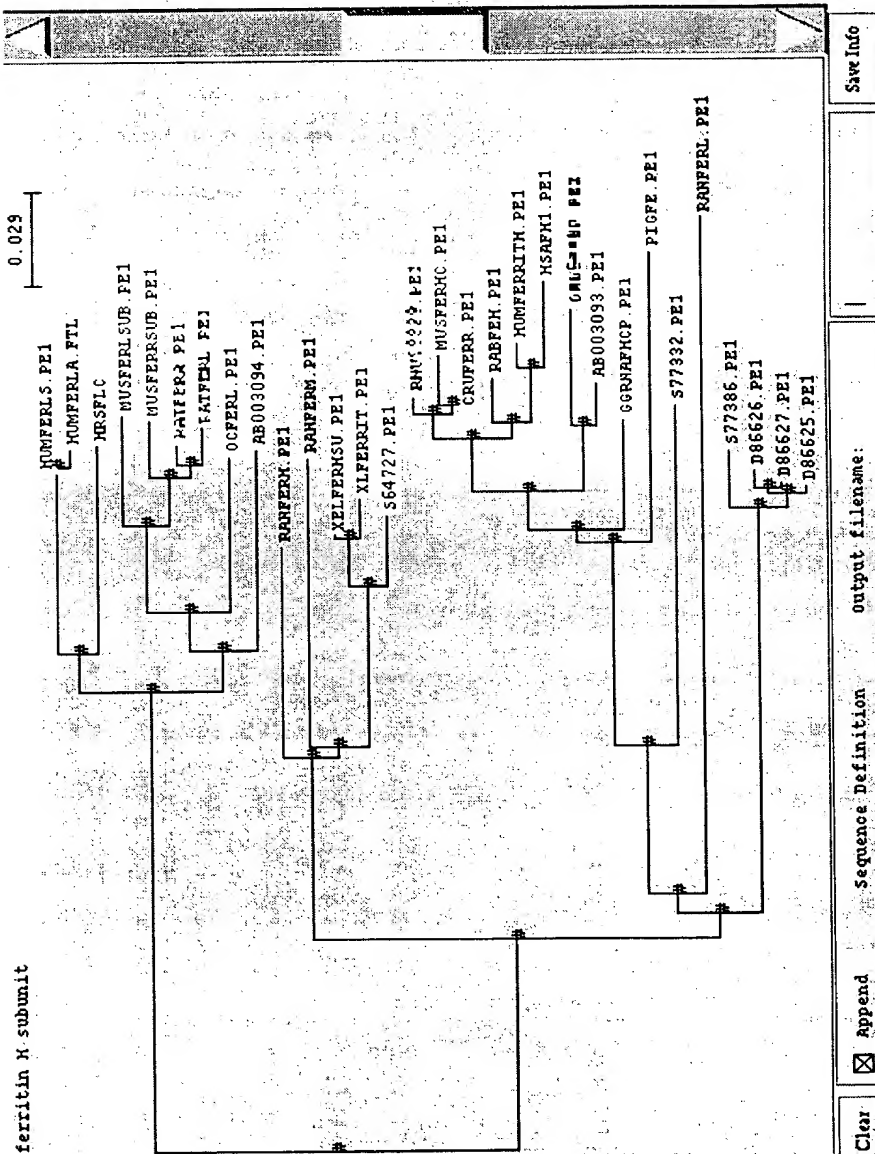


Figure 54



# Figure 55

ferritin X subunit



HOVERGEN  
Homologous Vertebrate Genes Data Base

Warning: Phylogenetic trees are unrooted!  
Select a gene or node (#) as outgroup to position the root (option="New outgroup")

- ☒ Get info
- ☒ Select for Alignment
- ☒ Select for Output
- ☒ New outgroup
- ☒ Swap nodes
- ☒ Sub-tree
- ☒ Reset tree

- ☐ Small leaf
- ☐ Branch lengths

tree display ... miscellaneous ...

New Tree

Legend for Taxon Color

species

Apply

Hovergen color file:

hovergen.color

Change Color Set

- ☐ HOMO SAPIENS
- ☐ MUS MUSCULUS
- ☐ RATTUS NORVEGICUS
- ☐ GALLUS GALLUS
- ☐ BOS TAURUS
- ☐ XENOPUS LAEVIS
- ☐ ORYCTOLAGUS CUNICULUS
- ☐ SUS SCROFA
- ☐ CAVIA PORCELLUS
- ☐ DANIO RERIO
- ☐ OVIS ARIES
- ☐ MAMMALIA
- ☐ Other

Save Info

output filename:

Sequence Definition

Append

Clear



# Figure 56

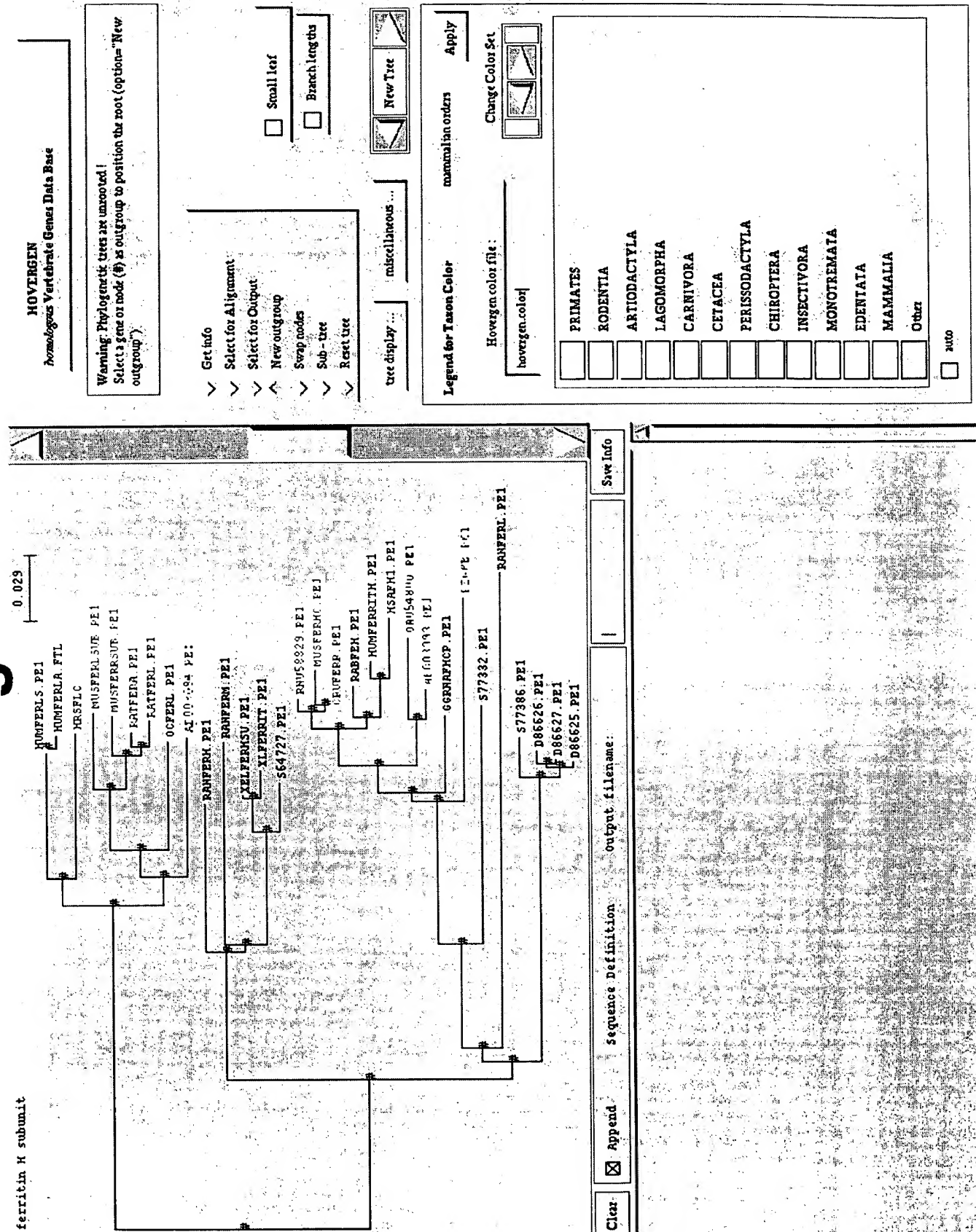


Figure 57

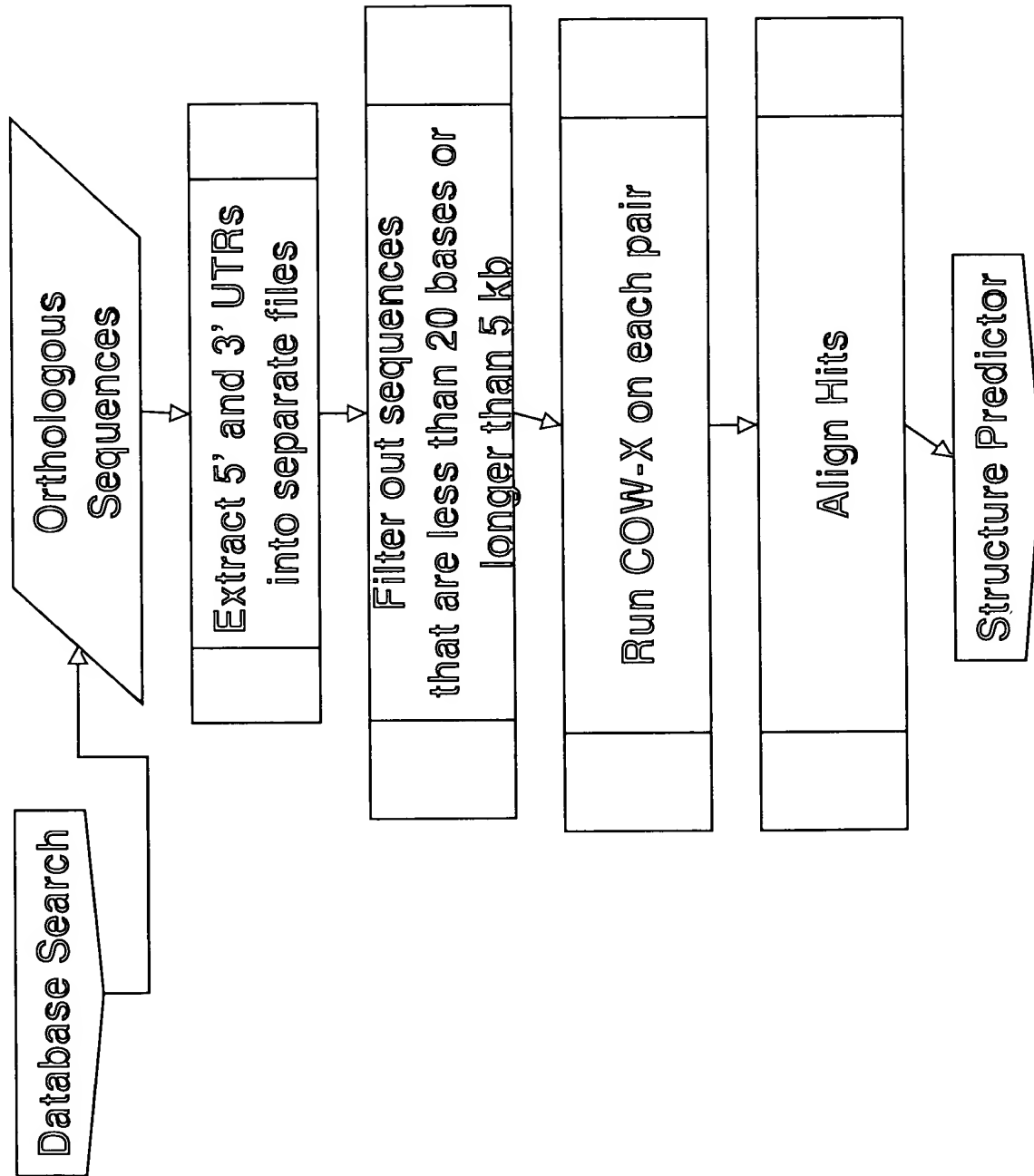


Figure 58

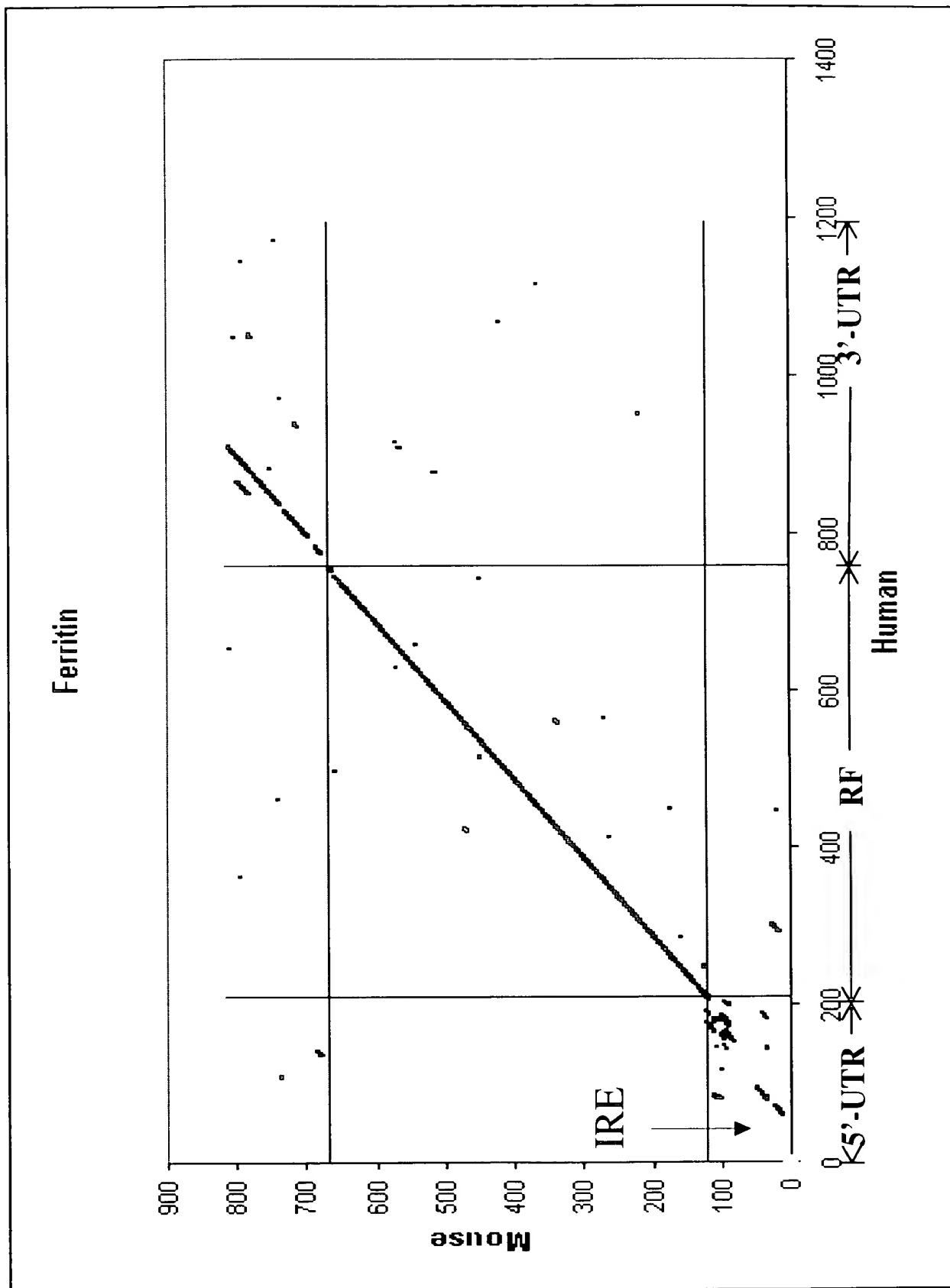
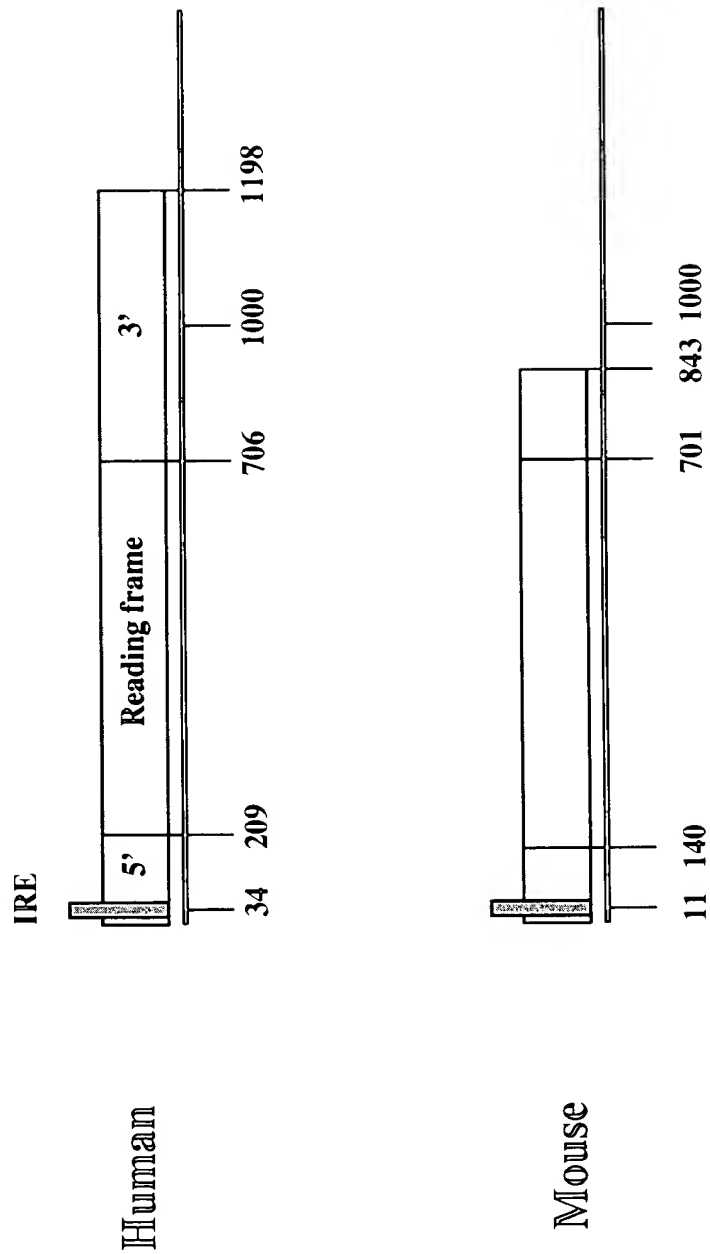


Figure 59



1000 900 800 700 600 500 400 300 200 100 0

Figure 60

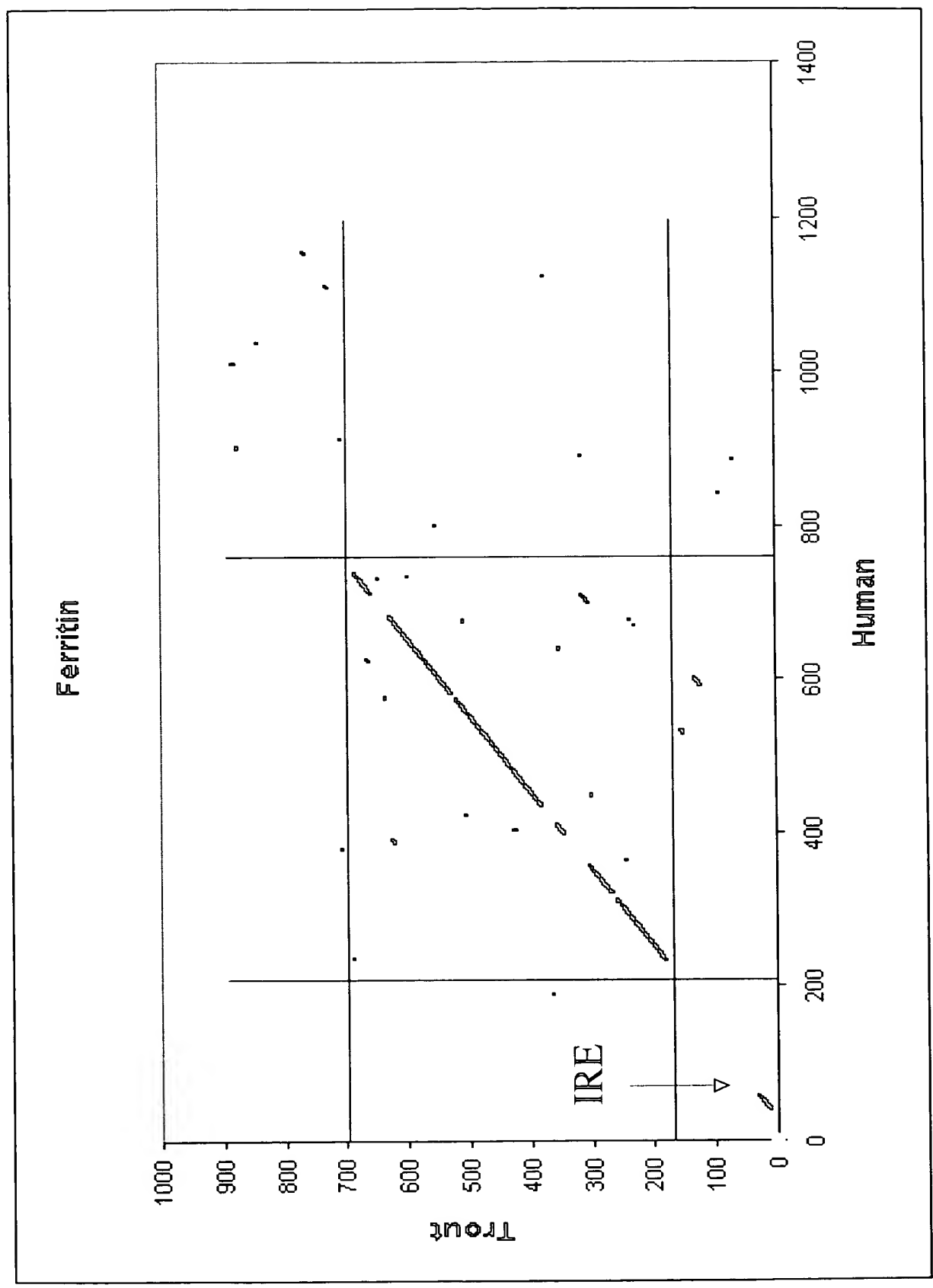
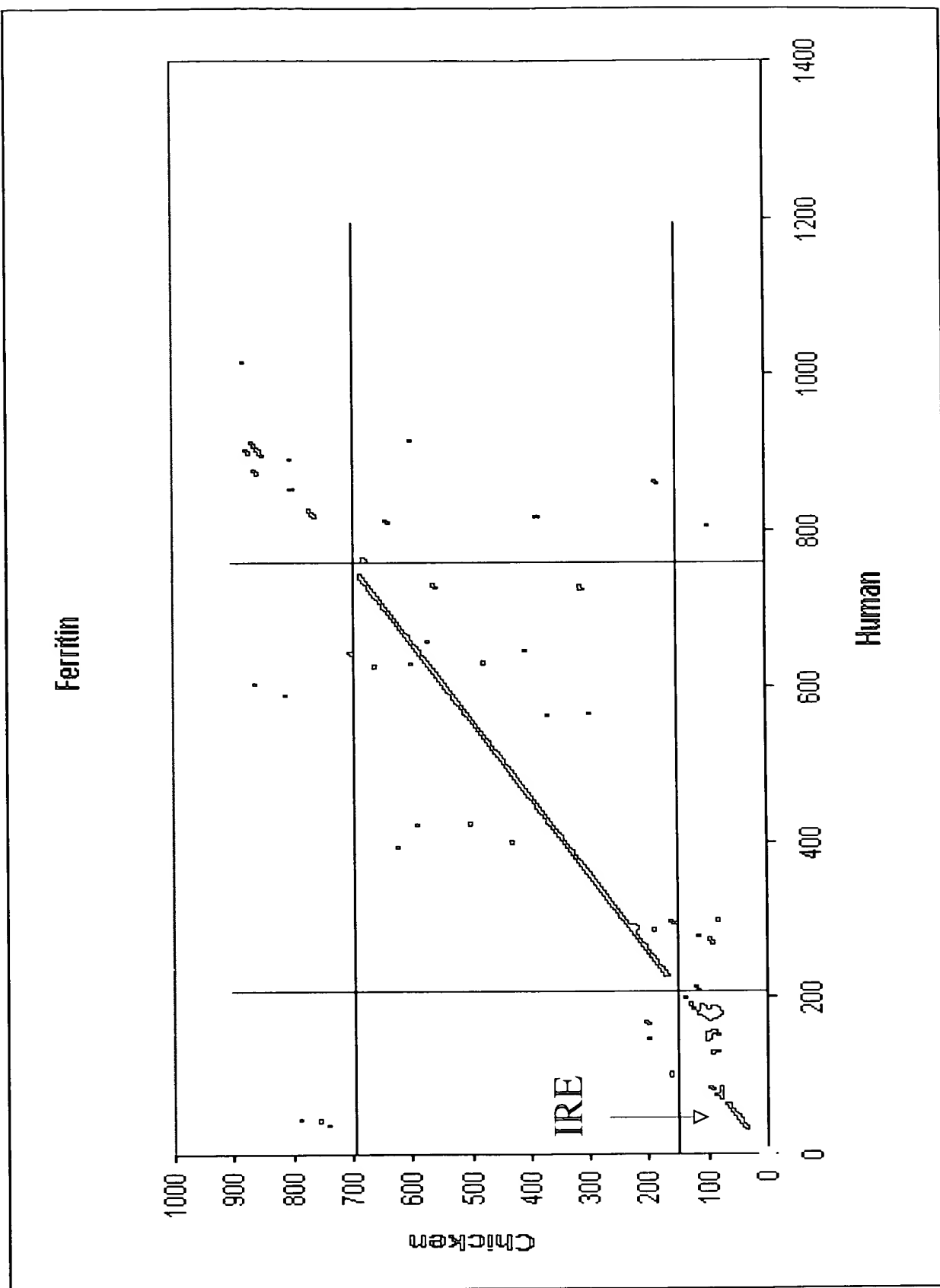


Figure 61



# Figure 62

## Conserved Region

Position: 507251 contig\_0419.seq15bp

Left SD: Left Mean: Discal det: 507251 fa

Right SD: Right Mean: Start: 507251 fa

Map directly to reference ☒ Threshold: 1.0

Number	Description	Left SD	Left Mean	Right SD	Right Mean	Start	End
1	Homo sapiens 5 prime UTR	-	-	-	-	-	-
2	Bos taurus 5 prime UTR [ori]	-	-	-	-	-	-
3	Ovis aries 5 prime UTR [orig]	-	-	-	-	-	-
4	Sus scrofa 5 prime UTR [ori]	-	-	-	-	-	-
5	Rattus norvegicus 5 prime U	-	-	-	-	-	-
6	Cricetulus griseus 5 prime U	-	-	-	-	-	-
7	Gallus gallus 5 prime UTR [	-	-	-	-	-	-
8	Salmo salar 5 prime UTR [o	-	-	-	-	-	-
9	Oncorhynchus mykiss 5 pri	-	-	-	-	-	-
10	Rana calespeiana 5 prime U	-	-	-	-	-	-
11	Xenopus laevis 5 prime UTR	-	-	-	-	-	-
12	Asterias forbesii 5 prime UT	-	-	-	-	-	-
13	Lymnaea stagnalis 5 prime	-	-	-	-	-	-
14	Aedes aegypti 5 prime UTR [	-	-	-	-	-	-
15	Drosophila melanogaster 5	-	-	-	-	-	-

His on sequence 507251

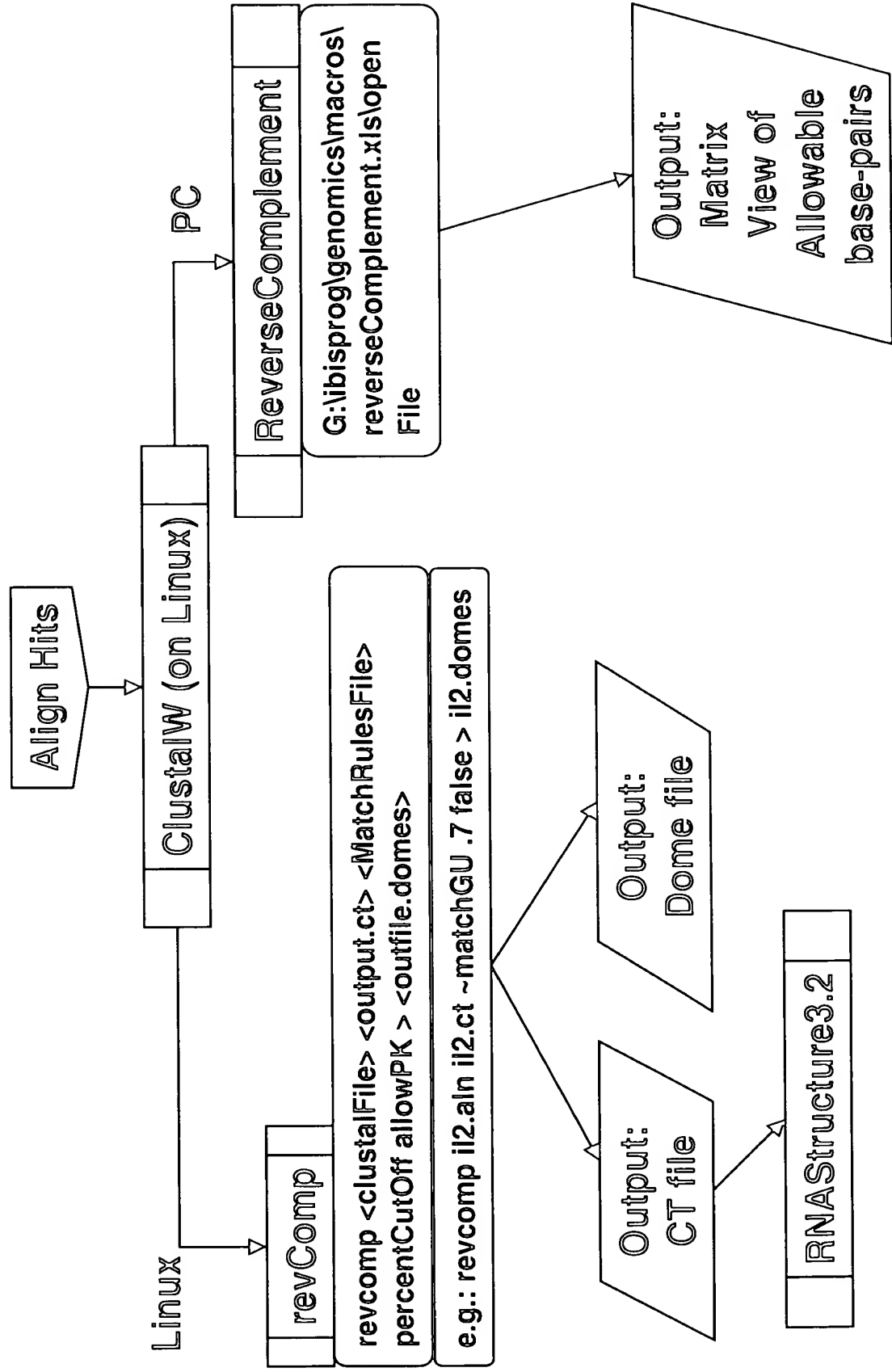
Start	End	Position	Length	Via	Alignment	Sequence
79	87	33	9	238858	-46	CTGCTTCAAA
261	270	35	10	238858	-226	GCTTCAACAG
353	368	127	16	238858	-226	CGAGCTGCCCAAGGC
359	369	99	11	238858	-260	GCCTCCGTCA
502	533	30	32	238858	-472	TTCTGCTTCAACAATGCTTGGACGGAACCCCG
524	534	117	11	238858	-407	ACCGCACCCCTC

# Figure 63

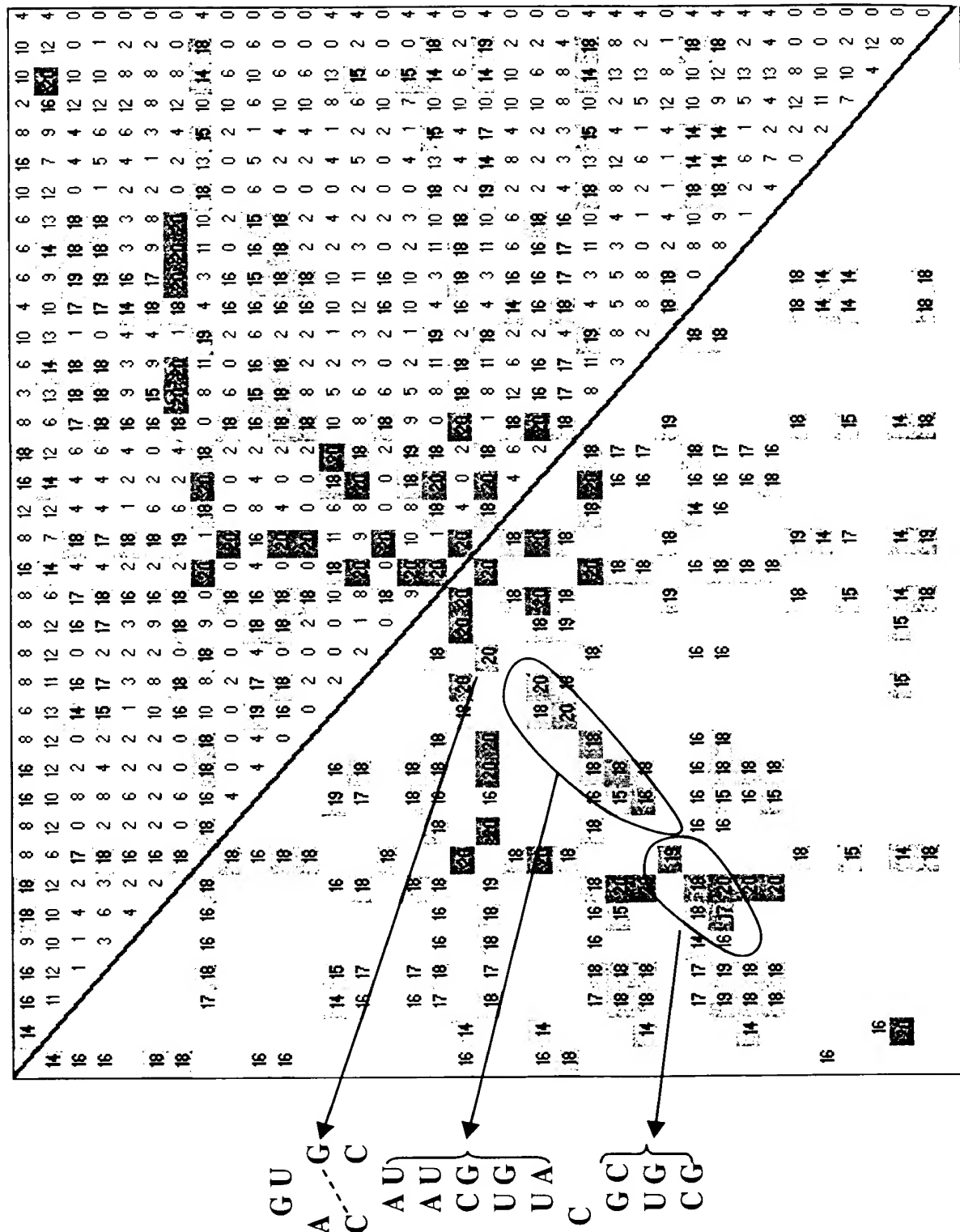
5p_xenopus_500_535_auto.aln [Read-Only]		A		E
1	CLUSTAL W (1.74) multiple sequence alignment			
2				
3				
4	gi 1752749 D86626	AGAAGTTGCTTCAACAGTGATTGAACGGAACTCCTC-		
5	gi 999126 S77386	AGTTCTTGCTTCAACAGTGATTGAACGGAACTCCTC-		
6	gi 213691 M12120	AGTTCTTGCTTCAACAGTGTTTGAACGGAAAC-CCTCT		
7	gi 238858 S64727	AGTTCTTGCTTCAACAGTGTTTGAACGGAAAC-CCTCT		
8	gi 286151 D15071	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGC-		
9	gi 507251 L20941	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGC-		
10	gi 191071 W99692	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGC-		
11	gi 2369860 Y14698	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGCC-		
12		*** ***** *	***** *	*
13				
14				
15				



Figure 64



# Figure 65



# Figure 66

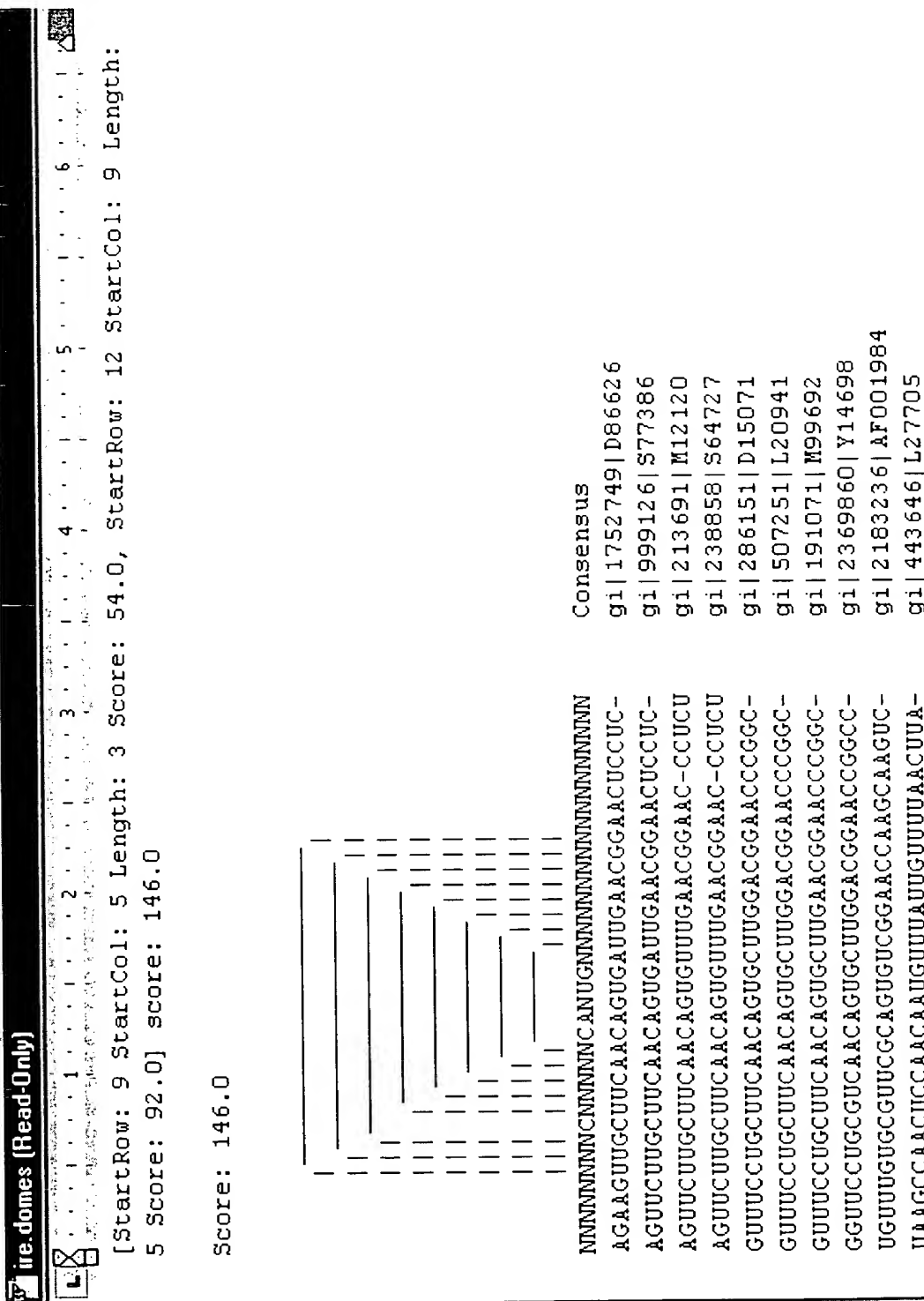


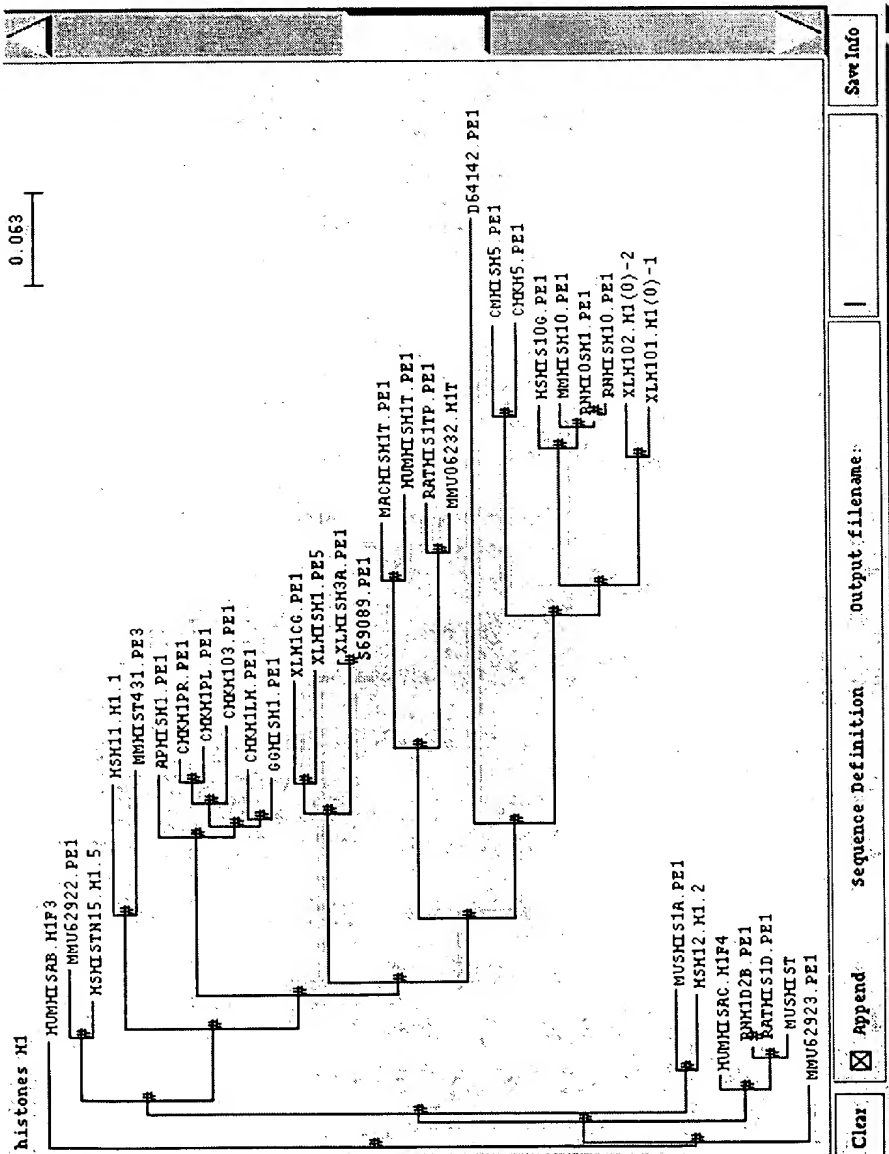
Figure 67

# IRE Structures for each species

<p>G-U A G C C</p> <p>A-U A-U C-G U-G U-A</p> <p>C G-C U-G C-G</p> <p>HUMAN PIG</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-A U-A</p> <p>C G-C U-G C-G</p> <p>HAMSTER MOUSE RAT</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-G G-A</p> <p>C G-C U-G C-G</p> <p>CHICKEN</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-A U-A</p> <p>C G-C U-G U-G</p> <p>TROUT SALMON</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-A U-A</p> <p>C G-C U-G U-G</p> <p>XENOPUS FROG</p>	<p>G U A G C C</p> <p>C-G G-U C-G G-U U-A</p> <p>C U-A U-A C-G</p> <p>FLY</p>	<p>G U A G C C</p> <p>C-G G-U C-G G-U U-A</p> <p>C U-A U-A C-G</p> <p>MOSQUITO</p>
---	---	---	--	--	---	--



# Figure 69



## HOVERGEN homologous Vertebrate Genes Data Base

Warning: Phylogenetic trees are unrooted!  
Select a gene or node (#) as outgroup to position the root (option= 'New outgroup')

- ☒ Get info
- ☒ Select for Alignment
- ☒ Select for Output
- ☒ New outgroup
- ☒ Swap nodes
- ☒ Sub-tree
- ☒ Reset tree

☐ Small leaf

☐ Branch lengths

tree display ...

miscellaneous ...

☒ New Tree

Legend for Taxon Color

vertebrate classes

Apply

Howzgen color file

Change Color Set

howzgen color

MAMMALIA

AVES

SAUROPSIDA

AMPHIBIA

LOBE-FINNED FISH AND TETRAPOD CLADE

ACTINOPTERYGII

CHONDRICHTHYES

PETROMYZONTIFORMES

MYXINIFORMES

Other

Save Info

Sequence Definition

output filename:

☒ Append

Clear

# Figure 70

Conserved Region

I:\HISTONE\cowx\_0416\seqs3p

Position:		Left Mean:		Left SD:	
Total hits:		Discarded:		Net:	
	Number	Description	Hits		
<input type="checkbox"/>	63477.fa	Gallus gallus 3 prime UTR [...]			
<input type="checkbox"/>	9788.fa	Pisaster brevispinus 3 prime...			
<input type="checkbox"/>	349586.fa	Volvox carteri 3 prime UTR [...]			
<input type="checkbox"/>	10044.fa	Pisaster ochraceus 3 prime ...			
<input type="checkbox"/>	9989.fa	Pycnopodia helianthoides 3 ...			
<input checked="" type="checkbox"/>	161381.fa	Psammochinus miliaris 3 pr...			
<input type="checkbox"/>	9614.fa	Lytechinus pictus 3 prime U...			
<input type="checkbox"/>	31967.fa	Homo sapiens 3 prime UTR ...			
<input type="checkbox"/>	64766.fa	Xenopus laevis 3 prime UTR...			
<input type="checkbox"/>	404465.fa	Styela plicata 3 prime UTR [...]			
<input type="checkbox"/>	342113.fa	Macaca mulatta 3 prime UT...			
<input type="checkbox"/>	797284.fa	Paracentrotus lividus 3 prim...			
<input type="checkbox"/>	287651.fa	Rattus norvegicus 3 prime U...			
<input type="checkbox"/>	2292939.fa	Mus musculus 3 prime UTR ...			
<input type="checkbox"/>	62730.fa	Cairina moschata 3 prime U...			
<input type="checkbox"/>	10251.fa	Strongylocentrotus purpuratu...			
<input type="checkbox"/>	62440.fa	Anas platyrhynchos 3 prime ...			
<input type="checkbox"/>	10338.fa	Solaster stimpsoni 3 prime ...			
<input type="checkbox"/>	515003.fa	Mus pahari 3 prime UTR [ori...			

# Figure 71

3p_xenopus_23_56_auto.aln [Read-Only]		A	
1	CLUSTAL W (1.74) multiple sequence alignment		
2			
3			
4	gi 10044 X54113	-TAAACAAAACGGCTCTTTTCAGAGCCACCACTTC-	
5	gi 9788 X54112	-TAAACAAAACGGCTCTTTTCAGAGCCACCACTTC-	
6	gi 9989 X54114	-TAATCAAAAACGGCTCTTTTCAGAGCCACCACTTC-	
7	gi 10251 V01356	ATACACAAA-CGGCTCTTTTCAGAGCCACCAAC-	
8	gi 161381 M10558	ATACACAAA-CGGCTCTTTTCAGAGCCACCAAC-	
9	gi 9614 X00628	TAACCAAAA-CGGCTCTTTTCAGAGCCACCAAC-	
10	gi 404465 S64499	-GACACAAAACGGCTCTTTTCAGAGCCACCA-ATCG	
11	gi 31967 X57129	AAACCCA-AAAGGCTCTTTTCAGAGCCACCACTGA-	
12	gi 515003 X80327	-CCCCACAAAGGCTCTTTTCAGAGCCACCACTGC-	
13	gi 2292939 Y12291	-CAATCCAAAAGGCTCTTTTCAGAGCCACCACTCC-	
14	gi 287651 X67320	-ACAACCCAAAGGCTCTTTTCAGAGCCACCCACAA-	
15	gi 342113 M97756	-AGAACCCAAAGGCTCTTTTAAGAGCCACCCACAT-	
16	gi 63477 X01752	-GATATCCAAAGGCTCTTTTAAGAGCCACCCACAC-	
17	gi 64766 X03017	-TATACCCAAAGGCTCTTTTCAGAGCCACCCACCC-	
18	gi 62440 X06128	-TAAACCCAAAGGCTCTTTTAAGAGCCACCCACTT-	
19	gi 62730 X14731	-TTAACCCAAAGGCTCTTTTCAGAGCCACCAACTT-	
20	gi 10338 X54115	-CAAAACCGAACGGCCCTTTTAGGCCACTACACTTT-	
21		* * * * *	* * *
22		NNNNNNNNANNGGCNCTTTTNNNNNNNNNNNNNN	
23			



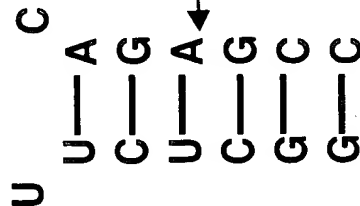
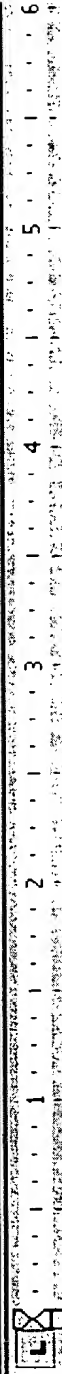


Figure 73

histone.domes (Read-Only)

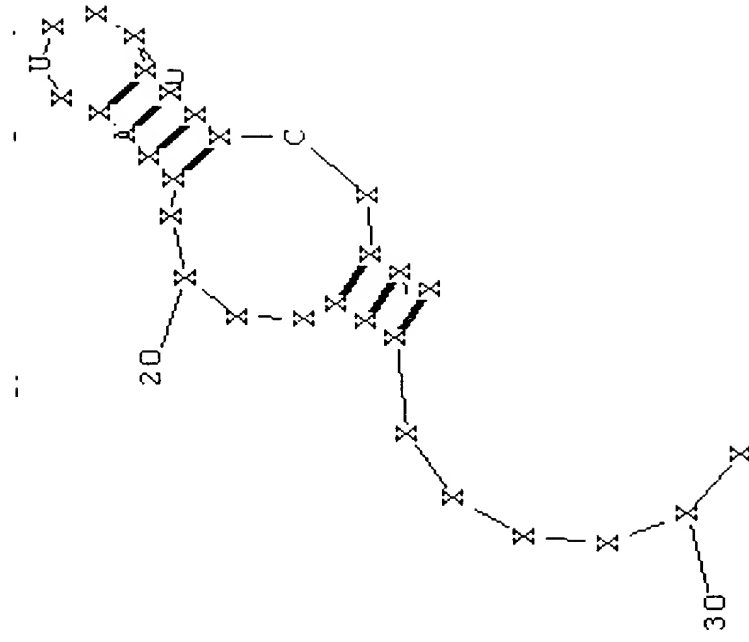


NNNNNNN	ANNGGCNCUUUUNNGNNNCNNNNNN	Consensus
-UAAACAAA	ACGGCUCUUUUCAGAGCCACCAUUC-	gi 10044 X54113
-UAAACAAA	ACGGCUCUUUUCAGAGCCACCAUUC-	gi 9788 X54112
-UAAUCAAA	ACGGCUCUUUUCAGAGCCACCAUUC-	gi 9989 X54114
AUACACAAA	-CGGCUCUUUUCAGAGCCACCAAC-	gi 10251 V01356
AUACACAAA	-CGGCUCUUUUCAGAGCCACCAAC-	gi 161381 M10558
UAACCAAAA	-CGGCUCUUUUCAGAGCCACCAUAC-	gi 9614 X00628
-GACACAAA	ACGGCUCUUUUCAGAGCCACCA-AUCG	gi 404465 S64499
AAACCCA-	AAAGGCUCUUUUCAGAGCCACCAUGA-	gi 31967 X57129
-CCCCACA	AAAGGCUCUUUUCAGAGCCACCAUGC-	gi 515003 X80327
-CAAUCCA	AAAGGCUCUUUUCAGAGCCACCAUCC-	gi 2292939 Y12291
-ACAACCCA	AAAGGCUCUUUUCAGAGCCACCACAA-	gi 287651 X67320
-AGAACCCA	AAAGGCUCUUUUAAGAGCCACCACAU-	gi 342113 M97756
-GAUAUCCA	ACGGCUCUUUUAAGAGCCACCAACAC-	gi 63477 X01752
-UAUACCCA	AAAGGCUCUUUUCAGAGCCACCAACCC-	gi 64766 X03017
-UAAACCCA	AAAGGCUCUUUUAAGAGCCACCAACUU-	gi 62440 X06128
-UUAACCCA	AAAGGCUCUUUUCAGAGCCACCAACUU-	gi 62730 X14731
-CAAAACCG	AACGGCCCCUUUUAAGGCCACUACACUUU-	gi 10338 X54115



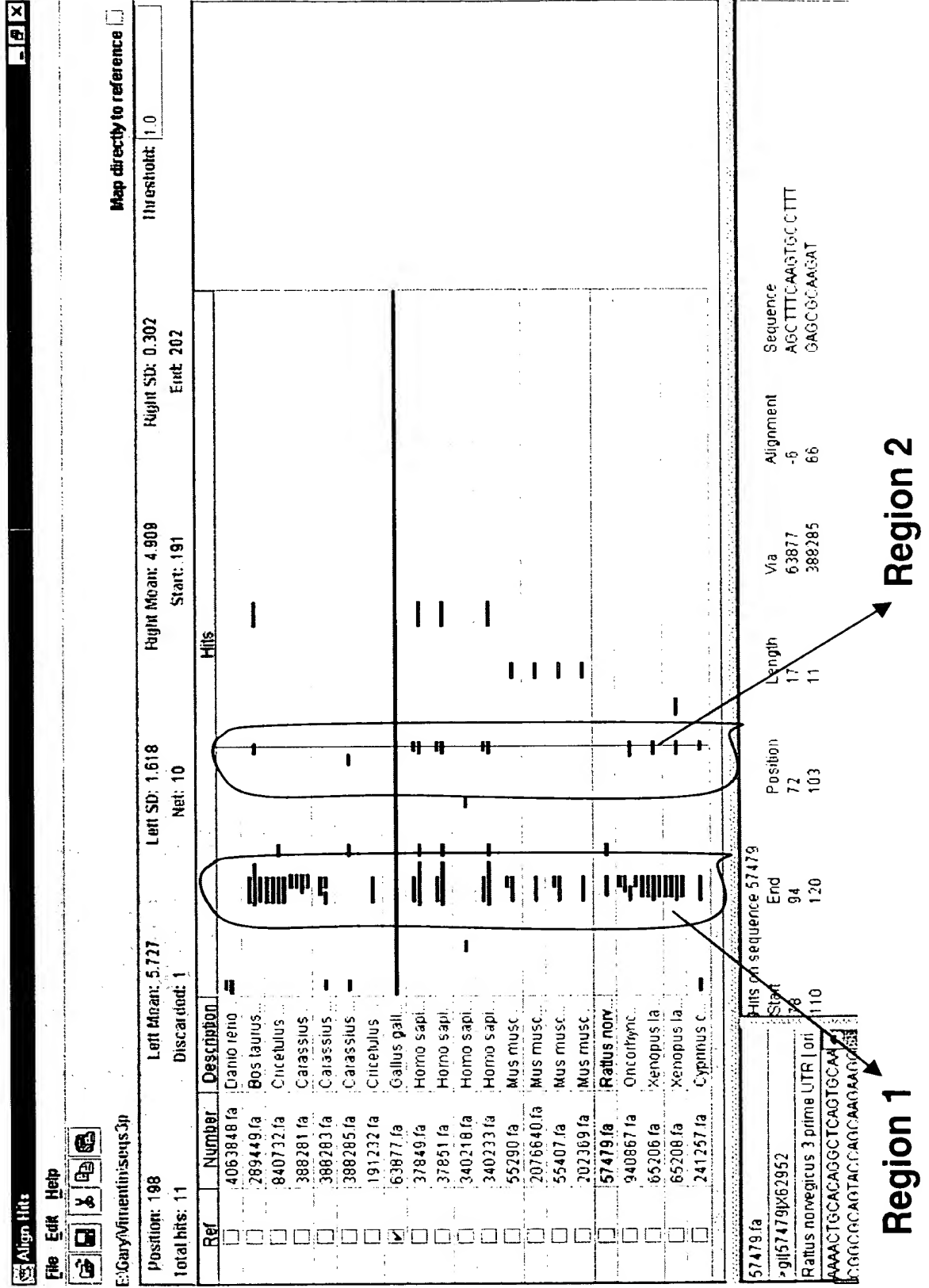
[illegible]

## Figure 75





# Figure 77

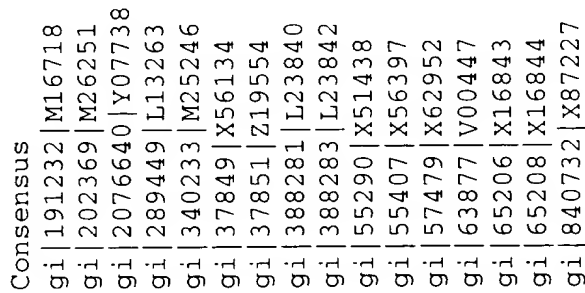


## Figure 78

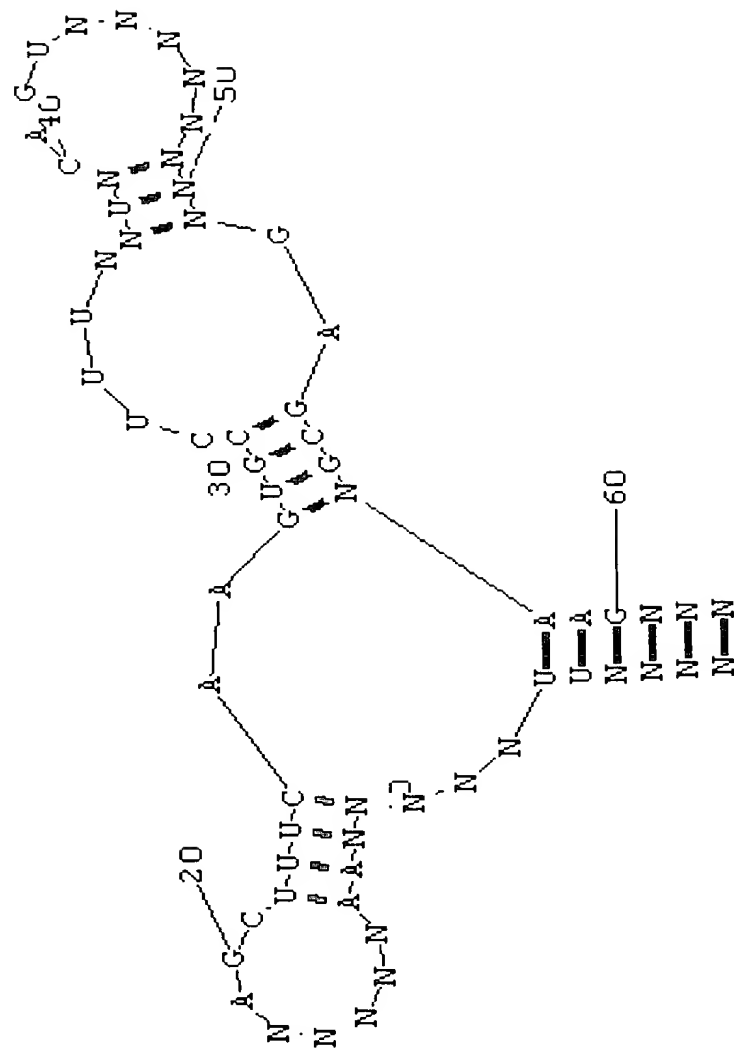
CLUSTAL W (1.74) multiple sequence alignment

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gi|202369|M26251      TATCTTAGGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
gi|2076640|Y07738     TATCTTAGGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
gi|289449|L13263      TATCTTAAGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCG-AAGATA
gi|340233|M25246      TATCTTAAGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
gi|37849|X56134       TATCTTAAGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
gi|37851|Z19554       TATCTTAAGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
gi|388281|L23840      CAACCCACAATAACTGCTTCAAGTGCCTTCTGCAGTTCAGAGTACAAAGCATTTGAGC
gi|388283|L23842      CTACCCACAATAACTGCTTCAAGTGCCTTCTGCAGTTCAGAGTACAAAGCATTTGAGC
gi|55290|X51438       TATCTTAGGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
gi|55407|X56397       TATCTTAGGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
gi|57479|X62952       TATCTTAGAATAAAAGCTTCAAGTGCCTTCTGCAGTTCAGGAGCGCAAGATA
gi|63877|V00447       TGTCTTAAAGGAAGAGCTTCAAGTGCCTTCTGCAGTTCAGGAGCGCAAGATT
gi|65206|X16843       ACTTTGAAGAAACAGCTTCAAGTGCCTTT-TGCAGTCAATGGAGAGCGCAAGATA
gi|65208|X16844       AATTTGAAGAAACAGCTTCAAGTGCCTTT-TGCAGTTAATGGAGAGCGCAAGATA
gi|840732|X87227      TATCTTAAGGAAACAGCTTCAAGTGCCTTCTGCAGTTTTTCAGGAGCGCAAGATA
```

Score: 445.0

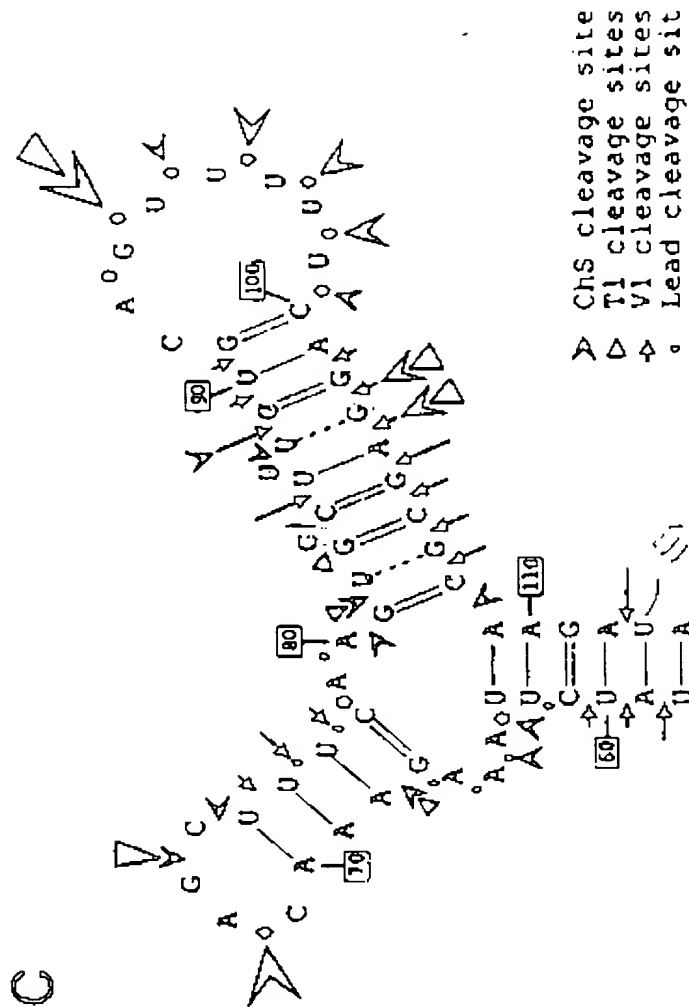






**Figure 80**

Figure 81



## Figure 82

CLUSTAL W (1.74) multiple sequence alignment

gi 241257 S76850	ACCACGATGT-CTGTAGTTTACACTGTTGAA
gi 289449 L13263	TTTACAACATAATCTAGTTTACCGAAGACGC
gi 340233 M25246	TTTACAACATAATCTAGTTTACAGAAAATC
gi 37849 X56134	TTTACAACATAATCTAGTTTACAGAAAATC
gi 37851 Z19554	TTTACAACATAATCTAGTTTACAGAAAATC
gi 388285 L23841	TCCACACTGGAGTAAACGAGGAAGAAATGAA
gi 63877 V00447	TTTACAATGGAGTCTAGTTTACAAATAGCAA
gi 65206 X16843	GCTTCCTTCT-GTCTAGTTTACAGACTGTAA
gi 65208 X16844	GCTTCCTTCT-GTCTAGTTTACAGACTATGT
gi 940867 Z50738	ACCACACTGA-GTCTAGTTTACACTTGGCT



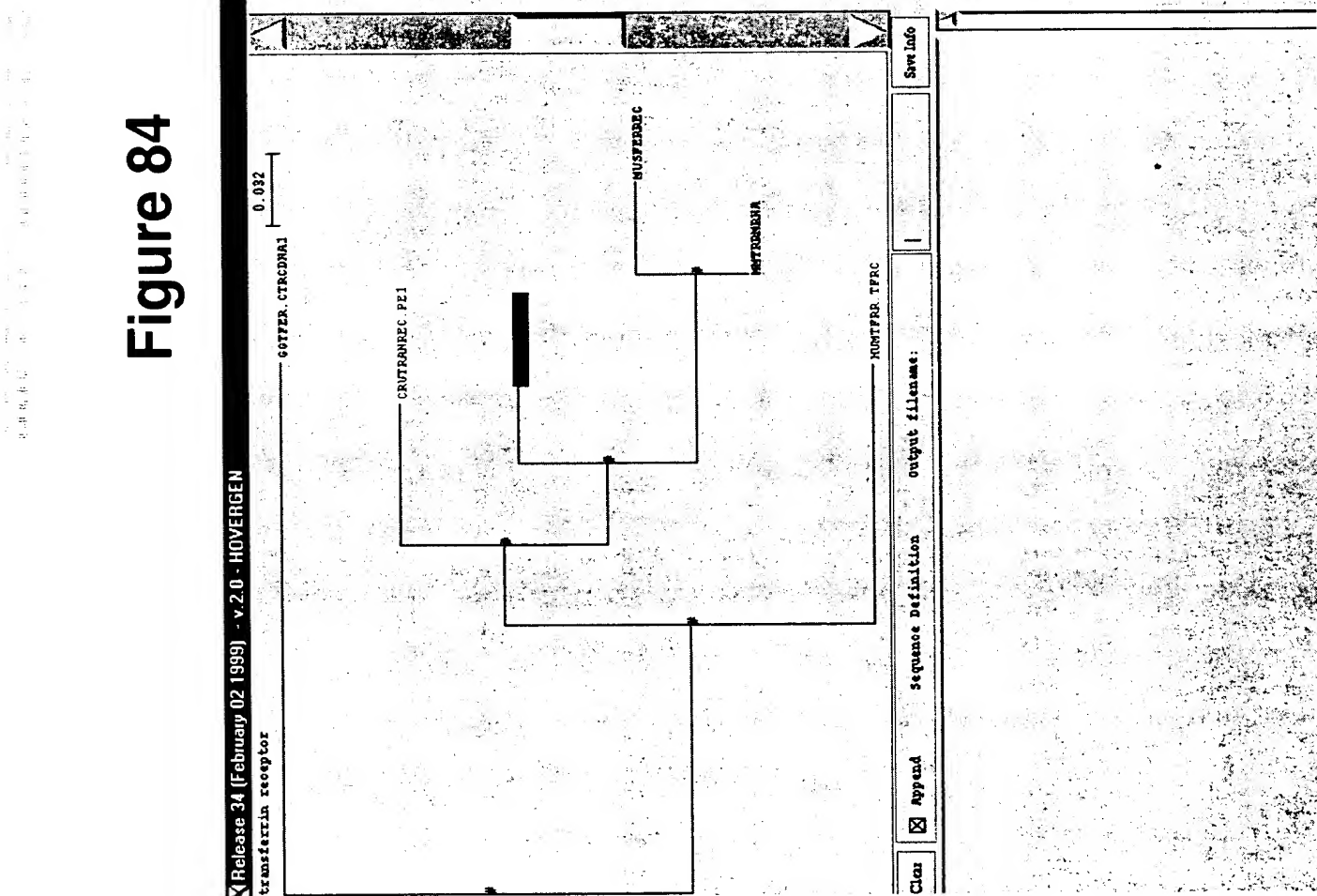
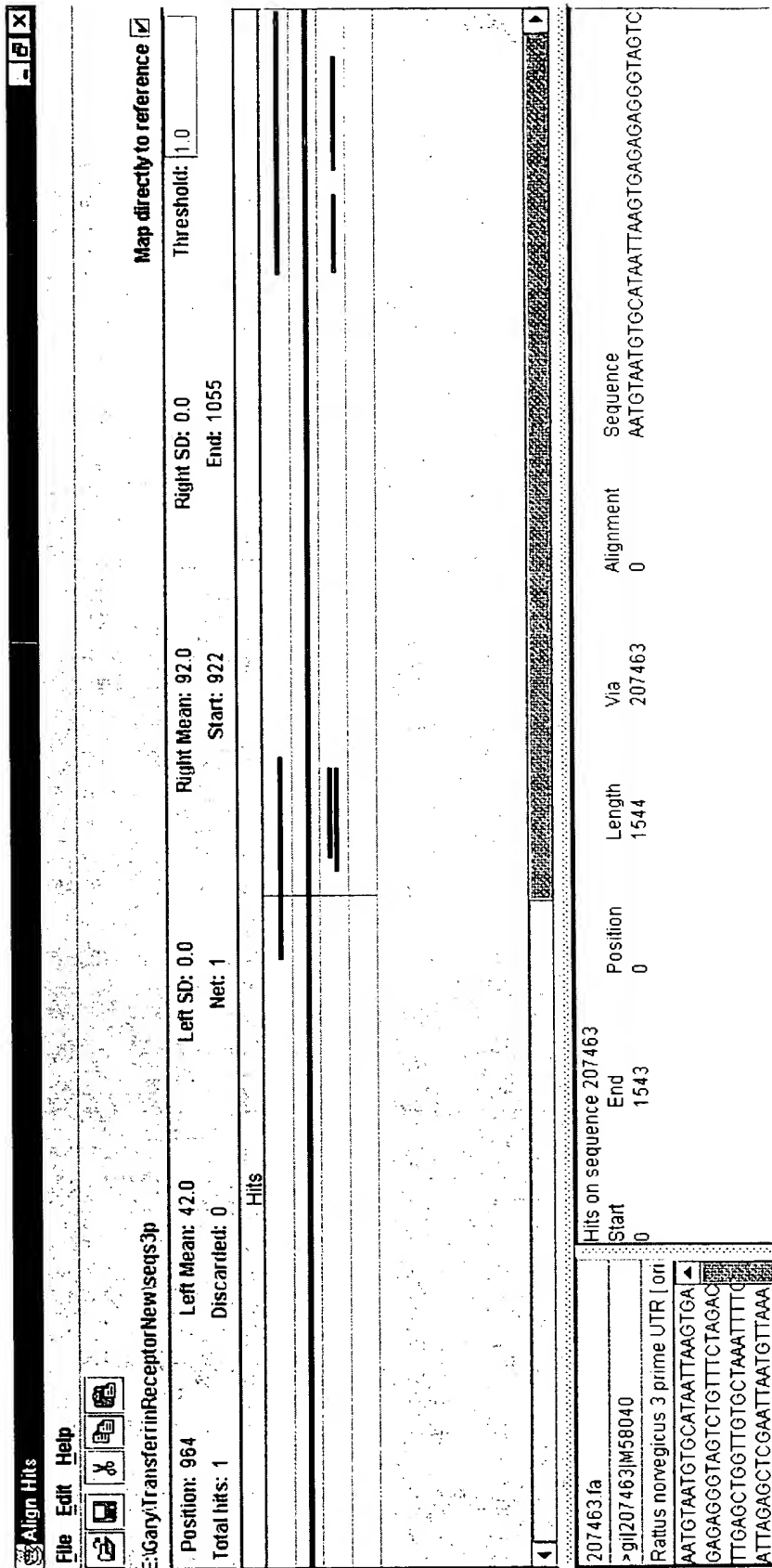
[illegible]

Figure 85



## Figure 86

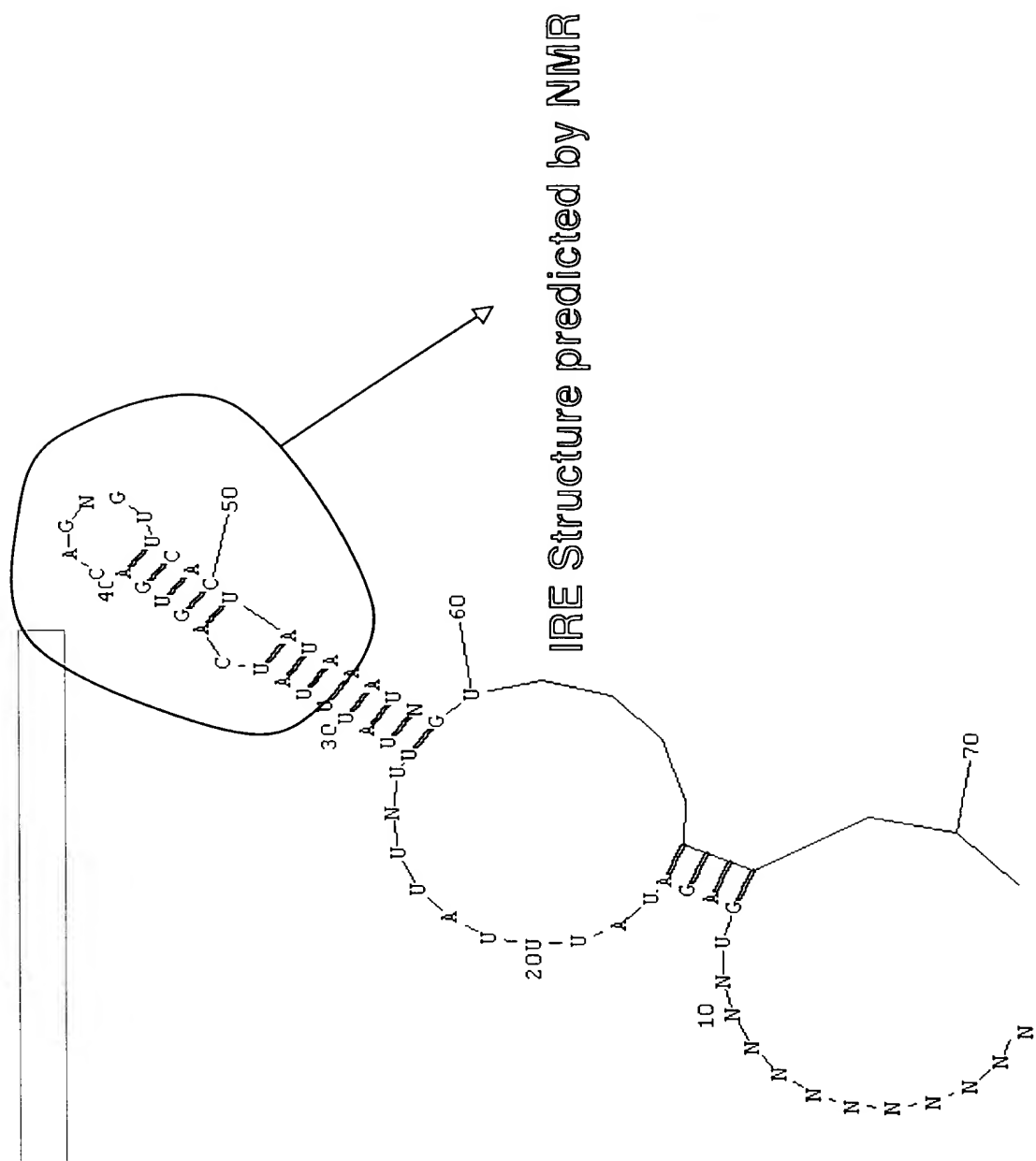
CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
GTTTGTGGCACTGAGATATTTATTGTTTATTATCAGTGACAGAGTTCACATATAAATAGTGTTTTAAAT
gi|37432|X01060
CCTTTTGGCACTGAGATATTTATTGTTTATTATCAGTGACAGAGTTCACATATAAATGGTGTTTTAAAT
gi|63357|X13753
-----
TGAGATATTTATTTTATTATCAGTGACAGCGTTCACATATAAATGGTGTTTTAT
```





Figure 88



## Align Hits

☒ Map directly to reference

Threshold: 1.0





[illegible]

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63357 fa	Hits on sequence 63357

	Start	End	Position	Length	Via	Alignment	Sequence
 <a href="#">g1633571x13753</a>	980	1048	865	69	207463	-115	GTTTTTTATAGAAGATAGGAGCGGGAAGCAGTGC
 Gallus gallus 3 prime UTR [origin]	989	1048	874	60	207463	-115	ATAGAAGATAAAGGAGCGGAAGCAGTGCCTTCCATA
 <a href="#">AACTTCTGACAGTGC</a> AAGCACGTG	1372	1423	1367	52	207463	-5	ACATTATCGGGGGCAGTGTCTTCCATAATGTGTAAT
 <a href="#">GTTTAAGGTACAGGGT</a> TAGGGAA	1439	1513	1432	75	207463	-7	TATATCGGAGGGCAGTGACCTCCCATATGTTGCATA

CCCACTCCCTACCCCTGCGCTC  
TGTAGAGGGGTGTTTTTTTTTT  
TTTTGGTAACAATCTCTCTGAC  
AAAGTTGAGCGTAAAAATTGAATC  
TCACCTTACACAATTCATAGAGC  
AGTTCTAAAGCAGTACTAAAAATTA  
GGATGAAATCTCTGACCAGGCTC

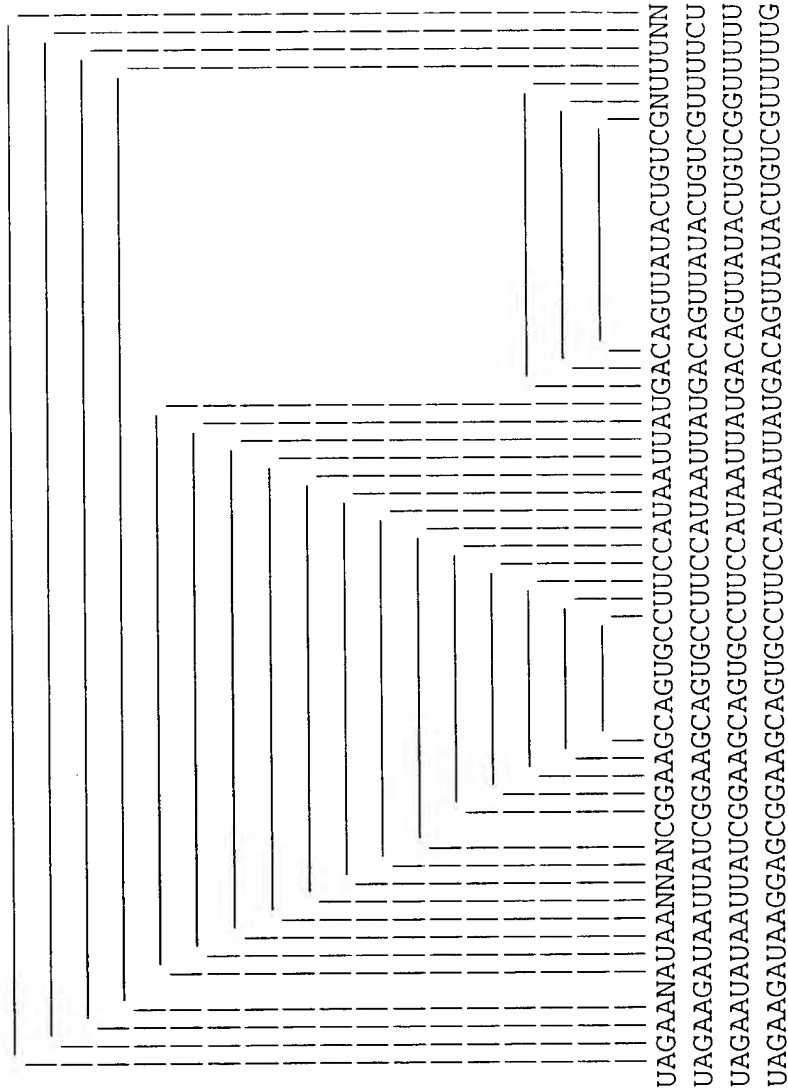
## Figure 90

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
TAGAAGATAATTATCGGAAGCAGTGCCCTCCATAATTATGACAGTTATACTGTCGTTTCT
gi|37432|X01060
TAGAATATAATTATCGGAAGCAGTGCCCTCCATAATTATGACAGTTATACTGTCGGTTTTT
gi|63357|X13753
TAGAAGATAAGGAGCGGAAGCAGTGCCCTCCATAATTATGACAGTTATACTGTCGTTTTTG
```

## Figure 91

Score: 115.0



Consensus  
gi | 207463 | M58040  
gi | 37432 | X01060  
gi | 63357 | X13753

Figure 92

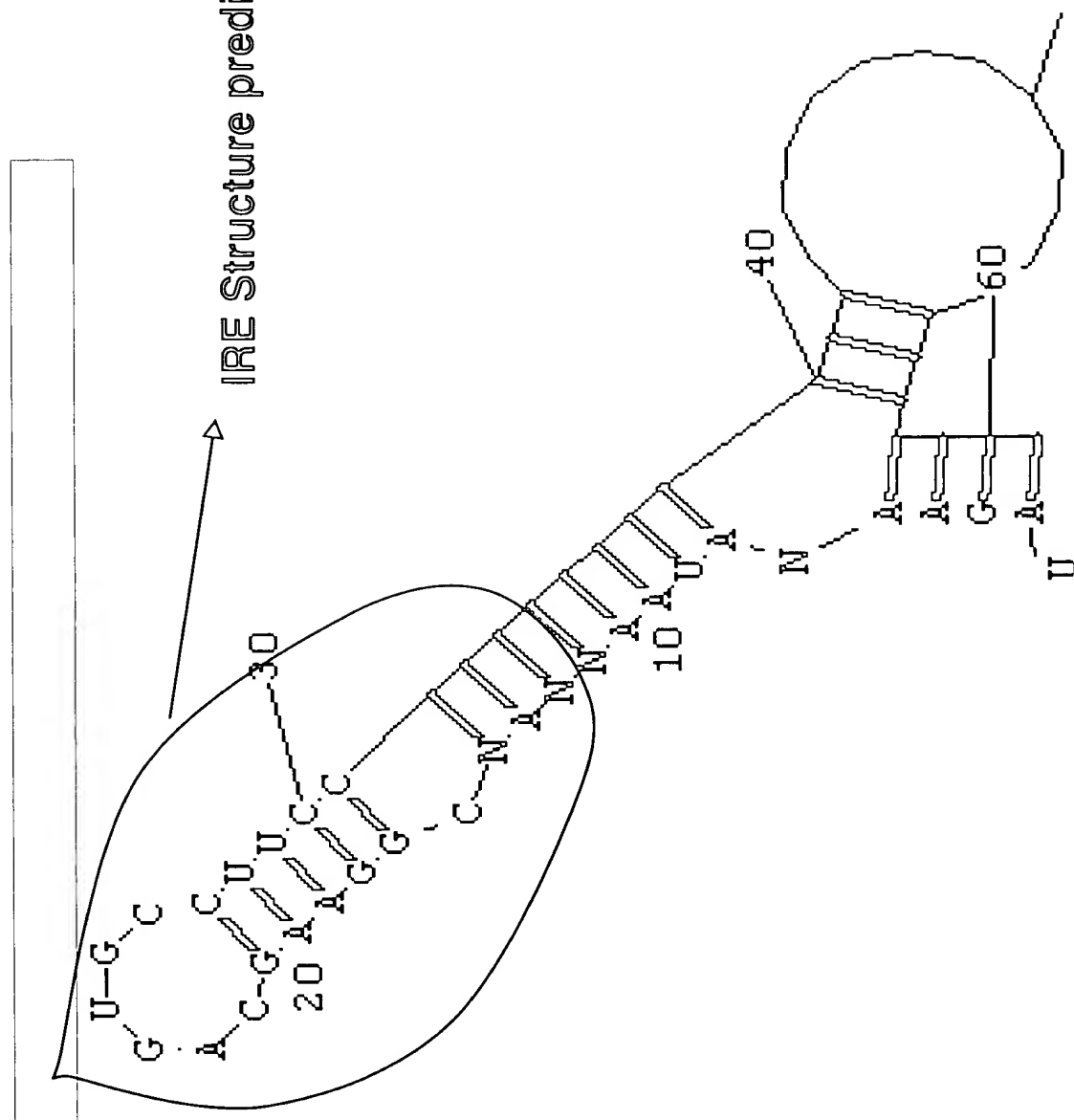
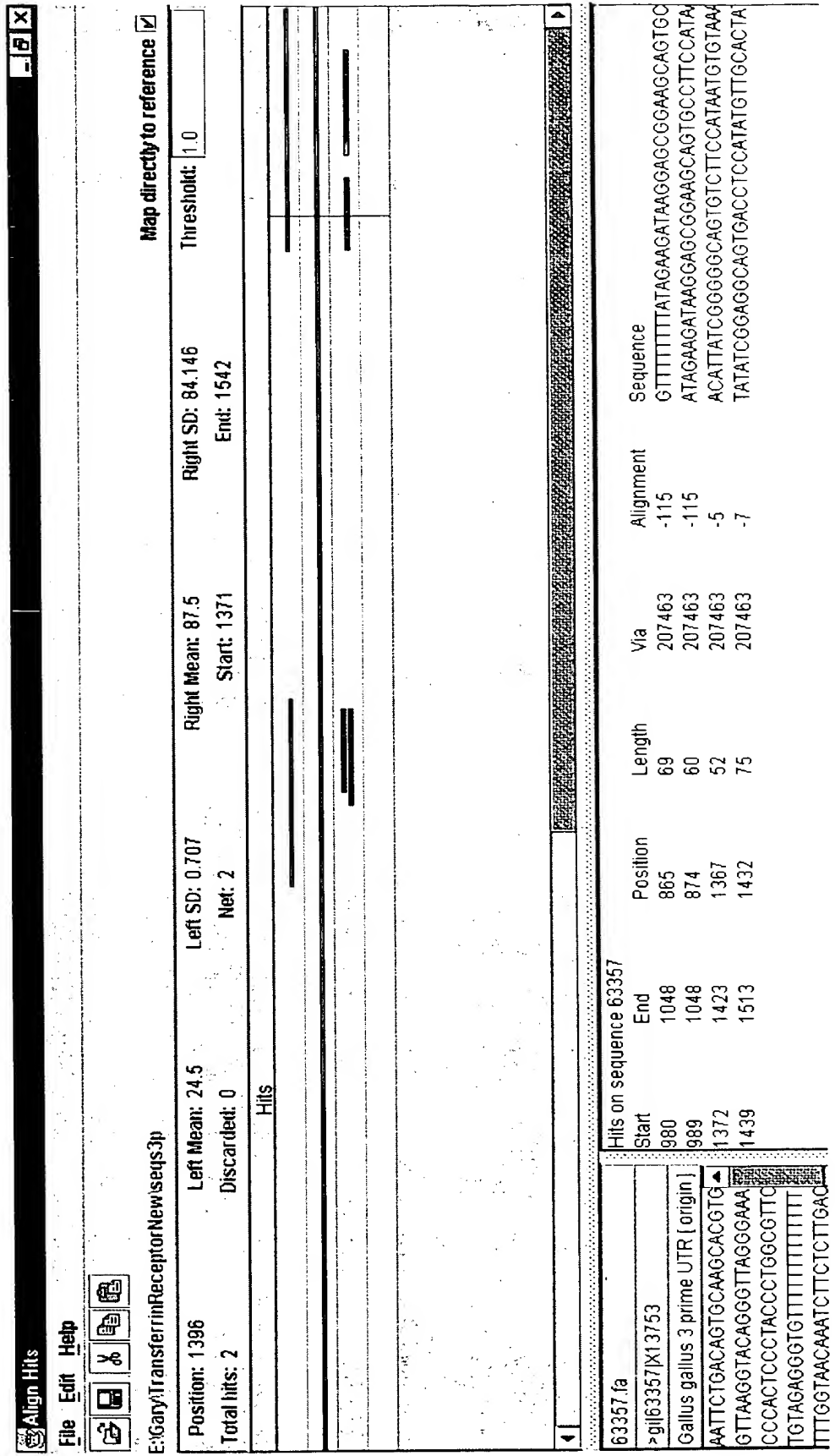


Figure 93



## Figure 94

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGAAACAAGGTAGTTTTT
gi|37432|X01060      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGAAACAAGGTAGTTTTT
gi|63357|X13753      ACATTATCGGGGGCAGTGTCTTCCATAATGTGTAAAGAAACAAGGTAGTTTTT
*****  *****  *****  *****  *****  *****  *****
```

Score: 108.0

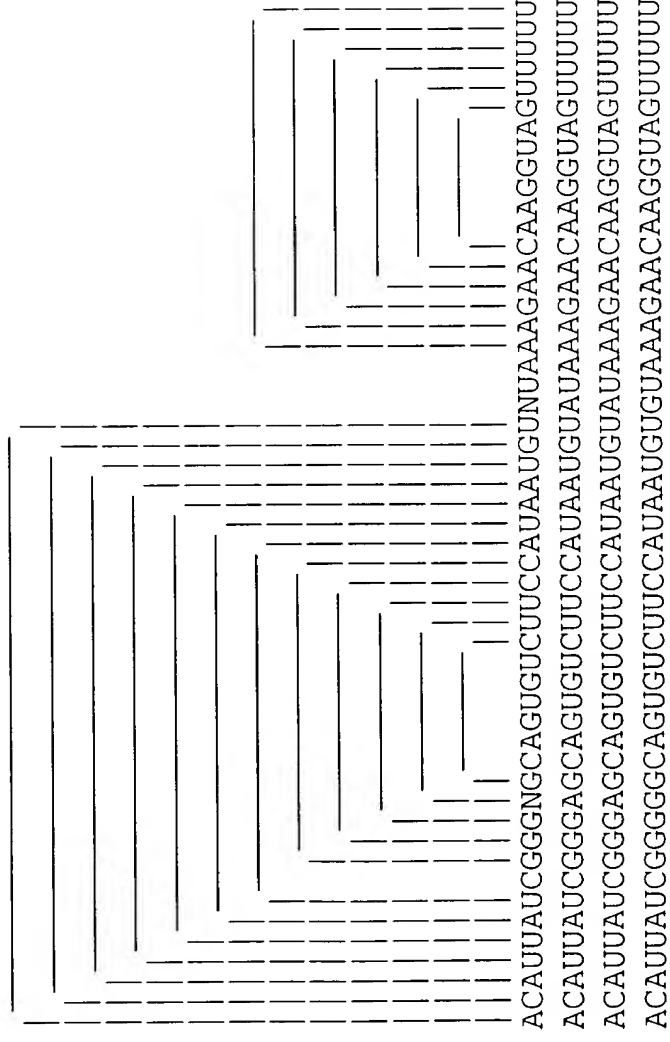
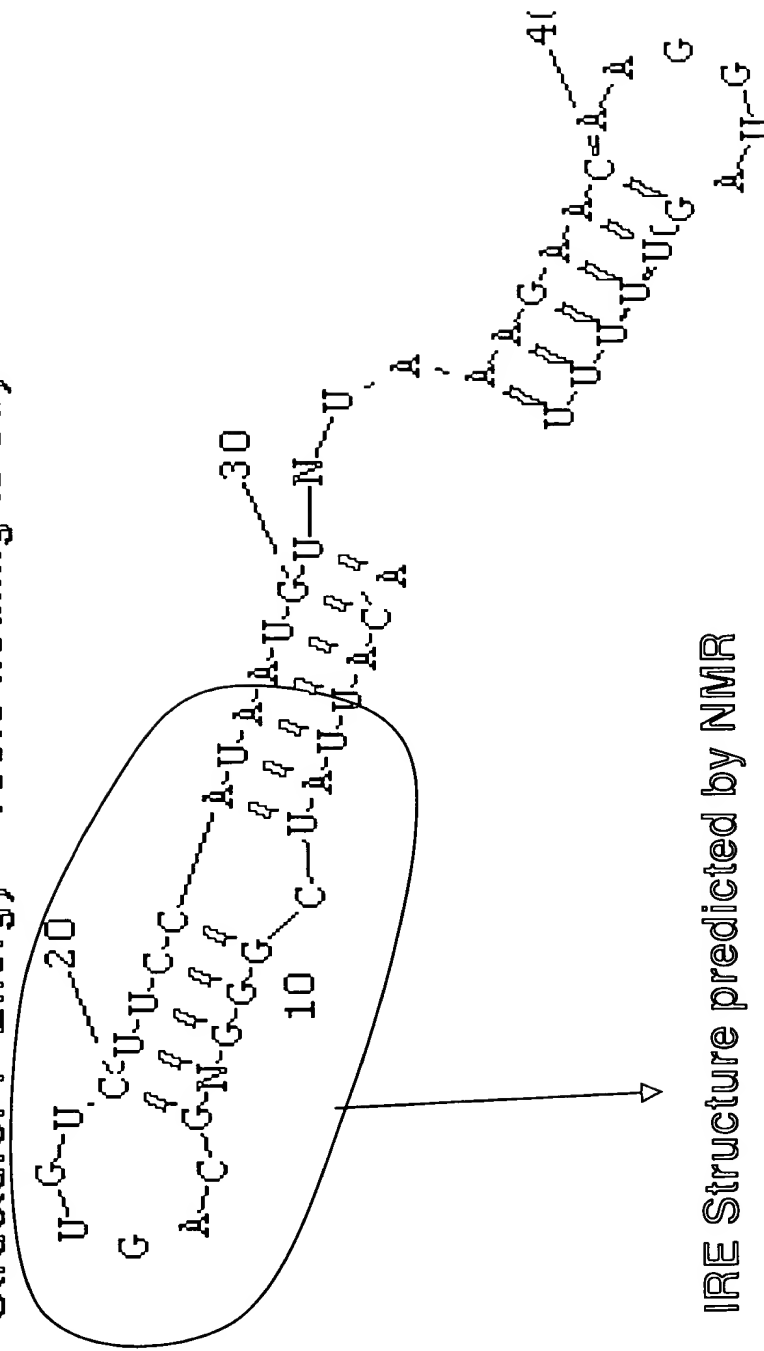


Figure 95



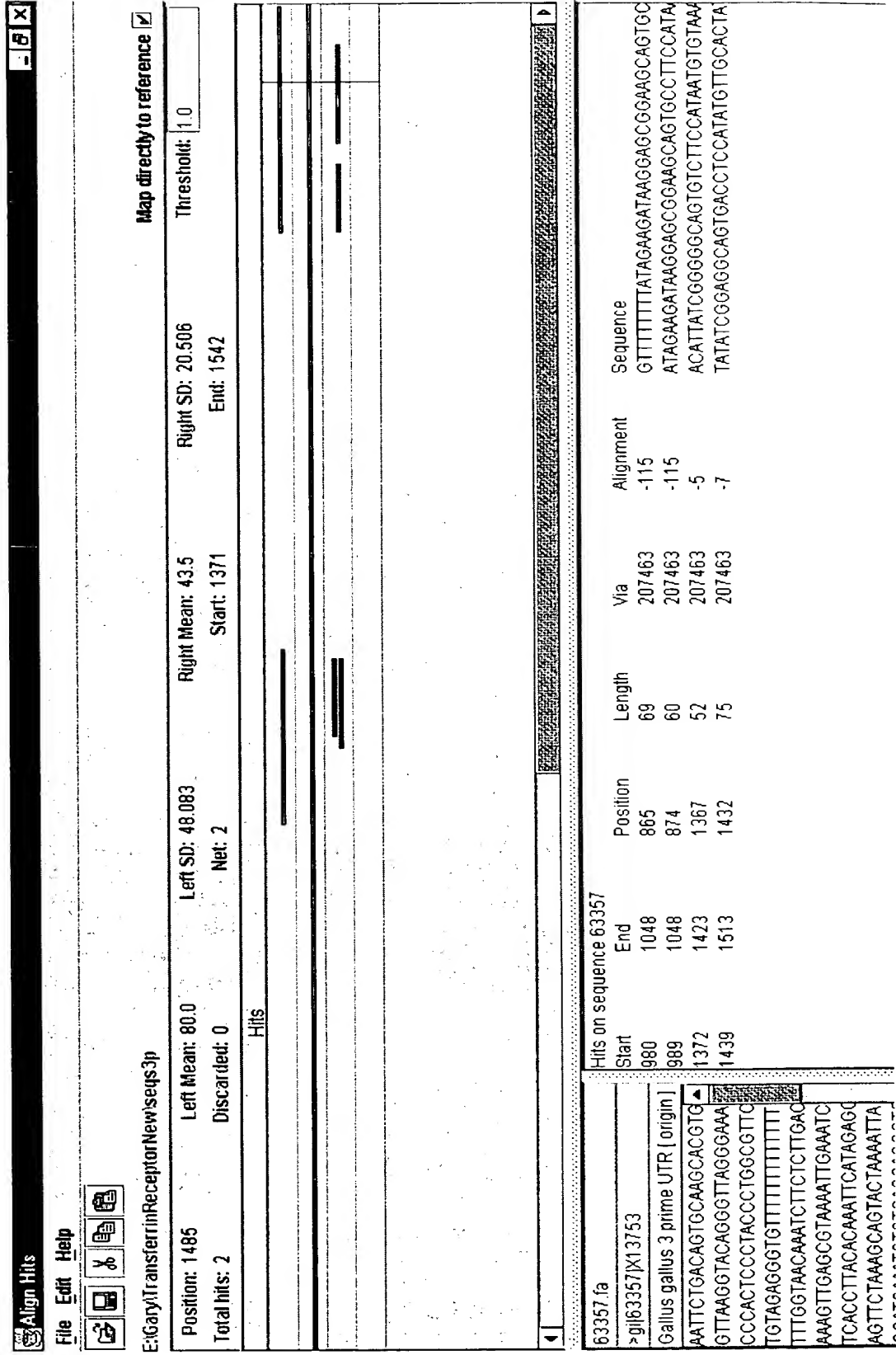
Figure 96

Structure: 1 Energy = 108.0 nothing to say



IRE Structure predicted by NMR

# Figure 97



## Figure 98

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      TATATCGGAGACAGTGACCTCCATATGTTACACTAAGGGTG
gi|37432|X01060      TGTATCGGAGACAGTGATCTCCATATGTTACACTAAGGGTG
gi|63357|X13753      TATATCGGAGGCAGTGACCTCCATATGTTGCACATATGGGGTG
* * * * *          * * * * *          * * * * *
```

## Figure 99

Score: 78.0

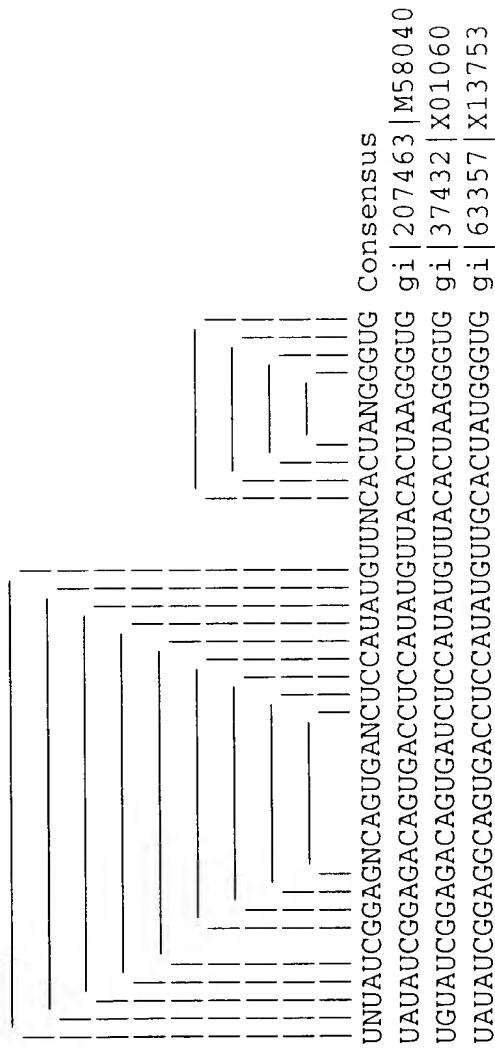
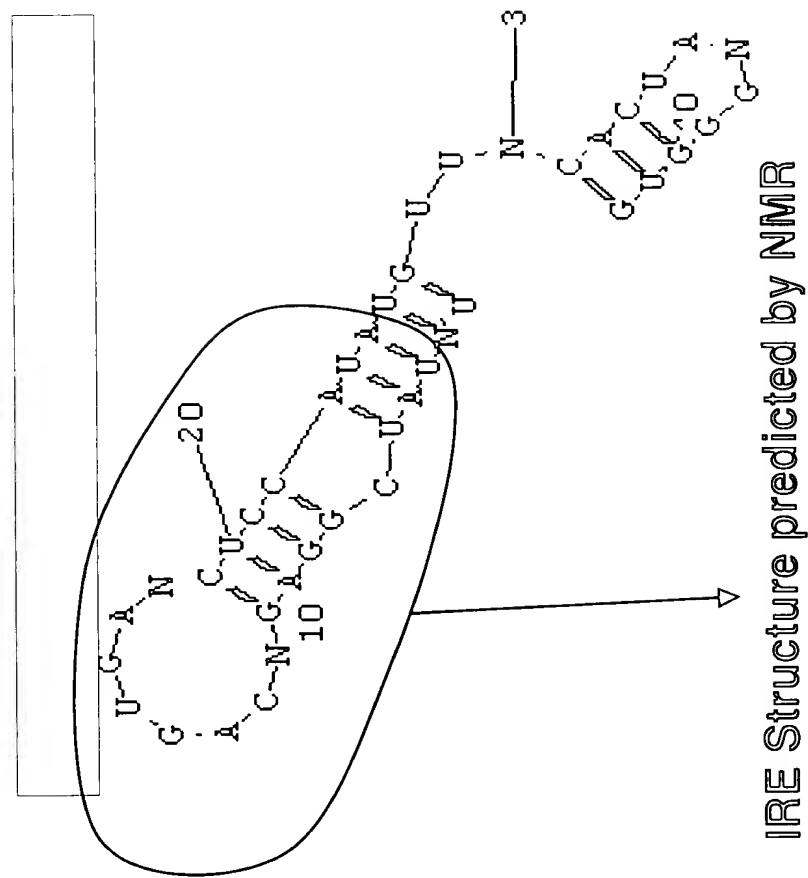


Figure 100



# Figure 101

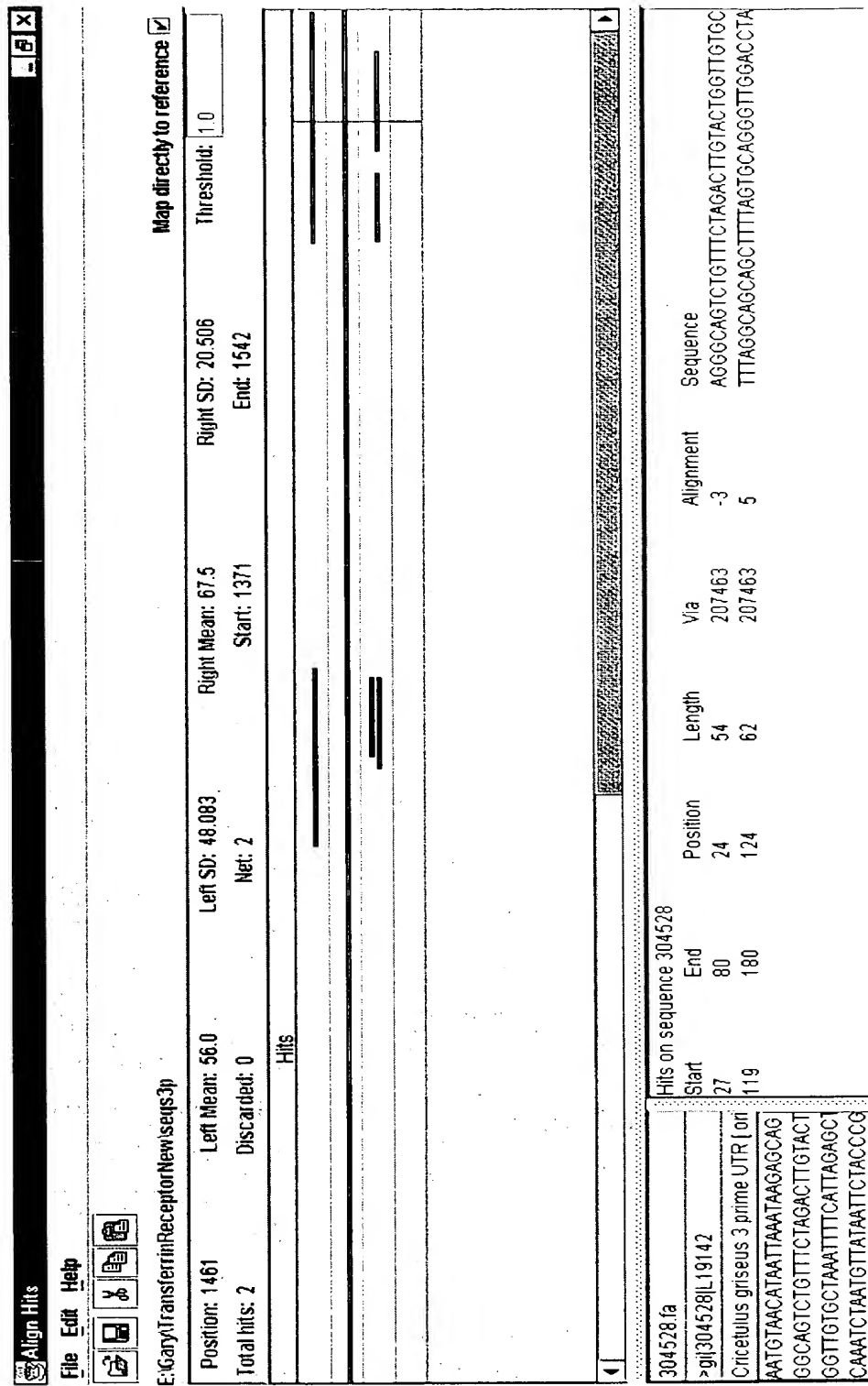


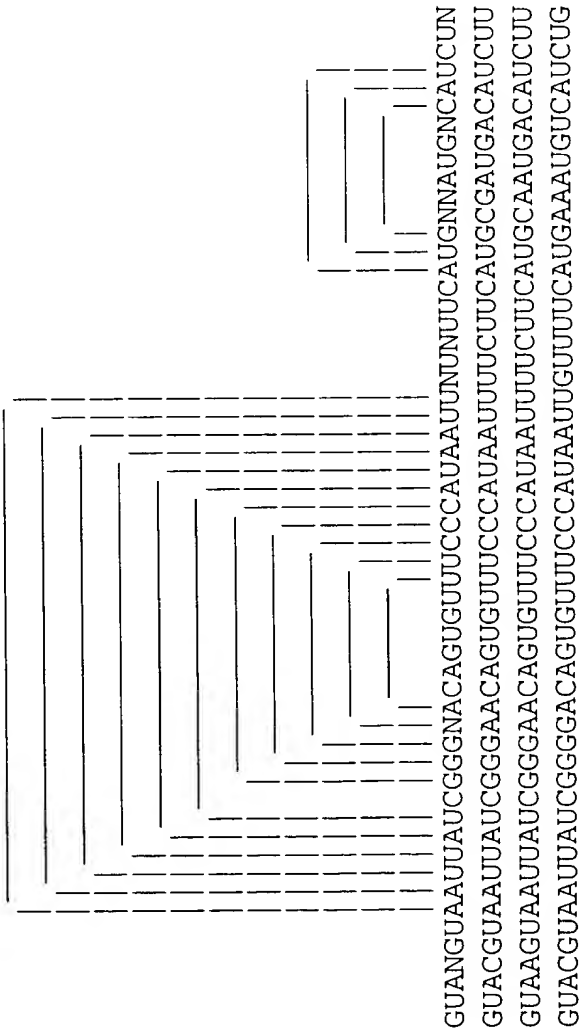
Figure 102

CLUSTAL W (1.74) multiple sequence alignment

gi 207463 M58040	GTACGTAATTATCGGGAACAGTGTTTCCCATAAATTTCTTCATGCGATGACATCTT
gi 37432 X01060	GTAAGTAATTATCGGGAACAGTGTTTCCCATAAATTTCTTCATGCAATGACATCTT
gi 63357 X13753	GTACGTAATTATCGGGGACAGTGTTTCCCATAAATGTTTTTCATGAAATGTCATCTG

## Figure 103

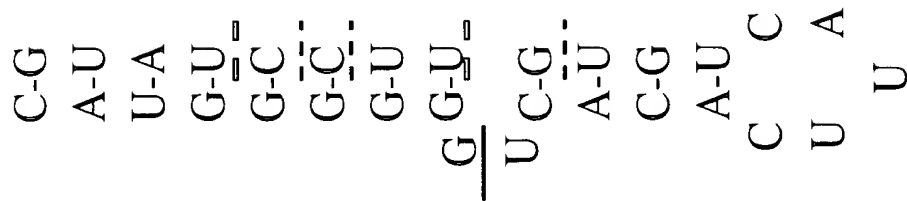
Score: 84.0



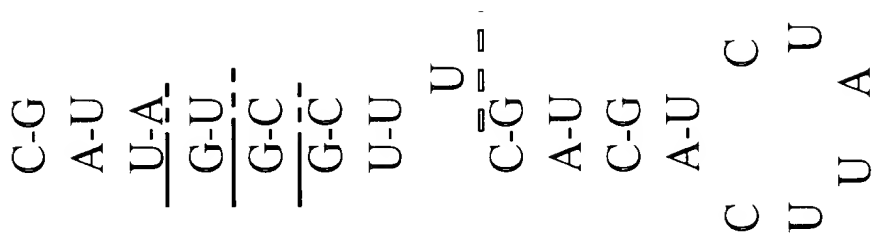




## Figure 105



404561



35135

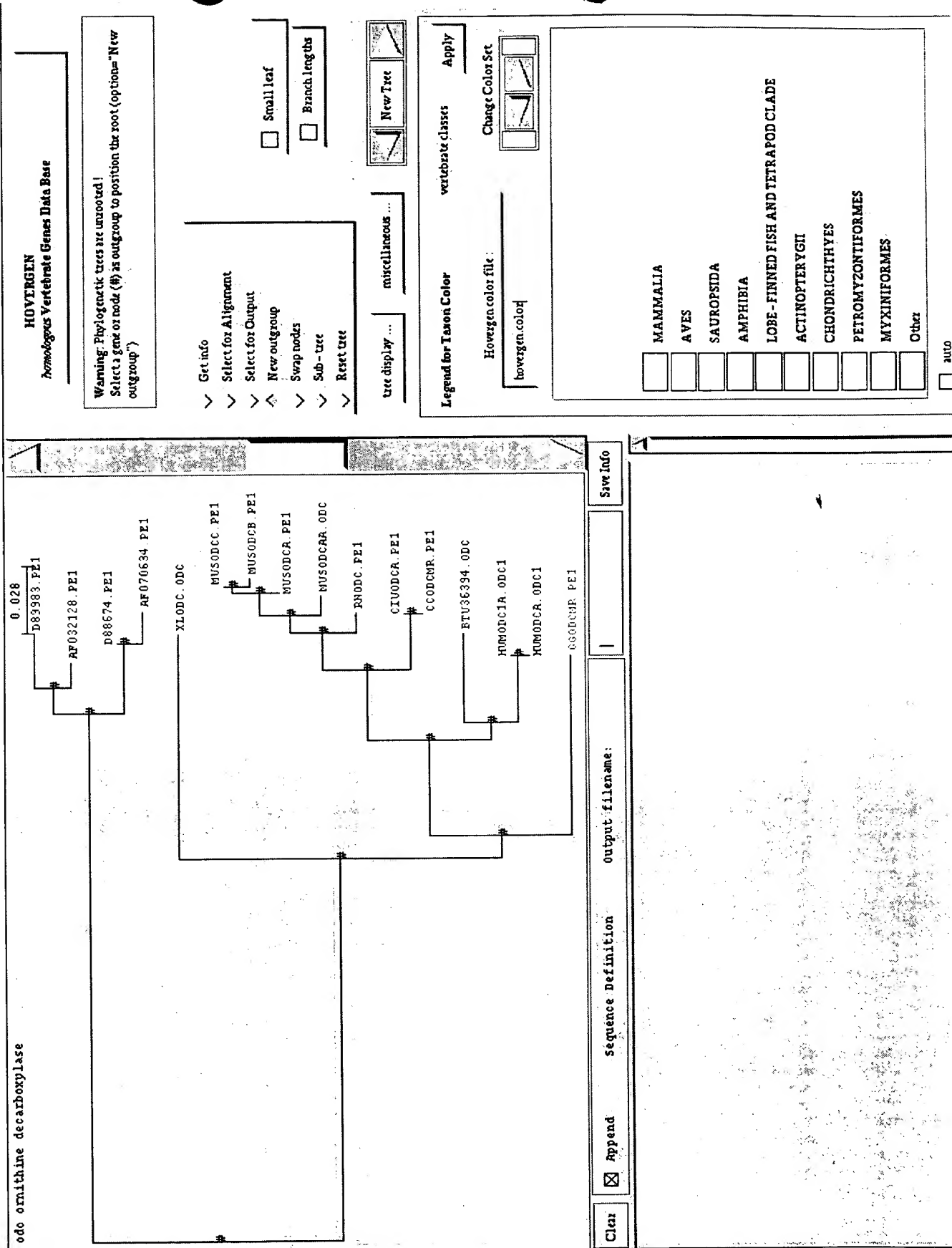
# Y ion

# Cion

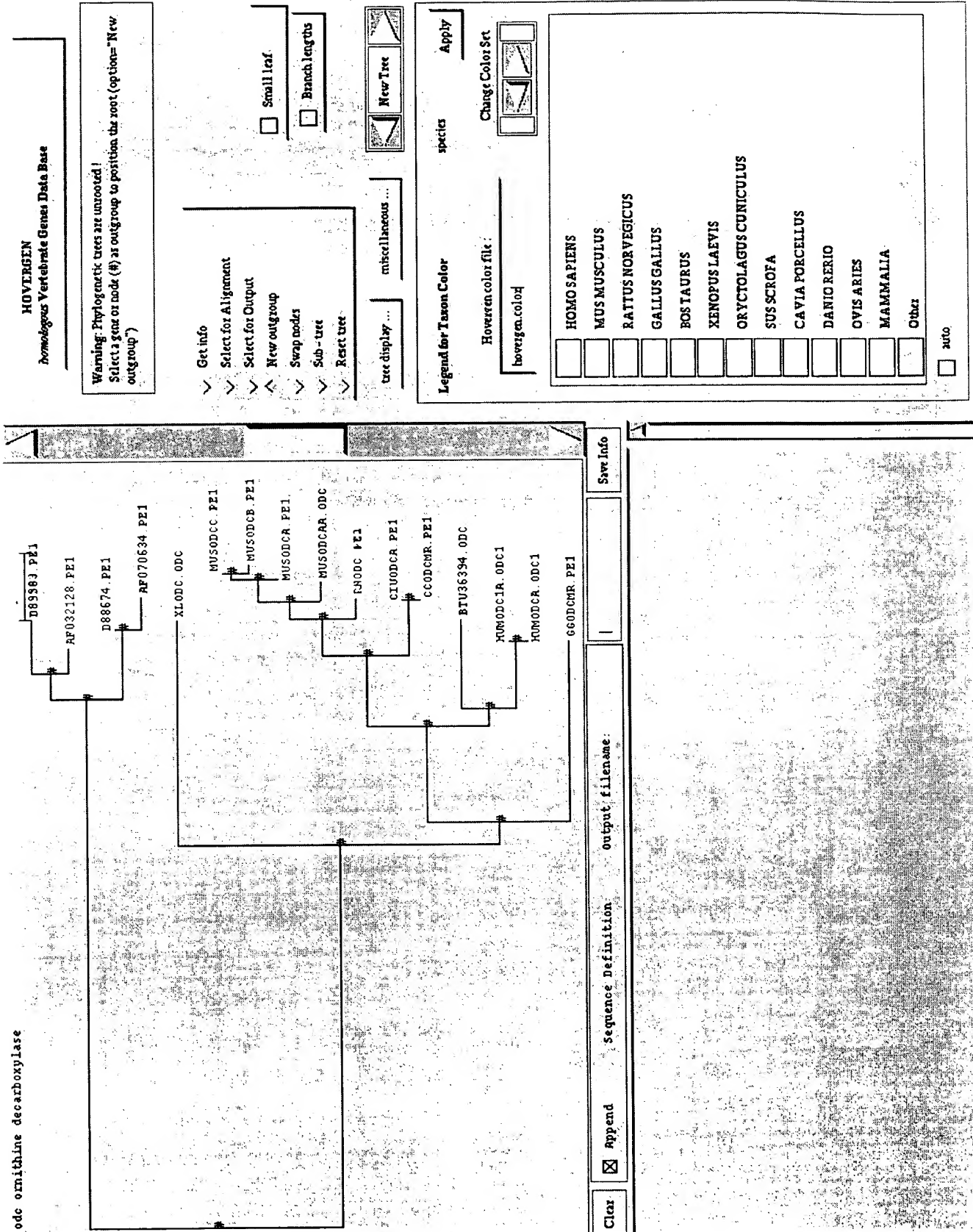
# Figure 106

CLUSTAL W (1.74) multiple sequence alignment		A	
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4	gi 163448 M92441	-ACTGGGAGATGGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAAATAT----	
5	gi 163448 M92441b	---TGGGAGATGGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAAATATTT--	
6	gi 200123 M87223	--CTAGAAGATGGGGG-TCACACTTAA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTG-	
7	gi 200123 M87223b	---TAGAAGATGGGGG-TCACACTTAA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTGT	
8	gi 205807 J04791	--CTAGGAGATGGGGG-TCACACTTAA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTT-	
9	gi 205807 J04791b	---TAGGAGATGGGGG-TCACACTTAA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTTA	
10	gi 35135 X55362	--CTAGGATATGGG---TCACACTTATCTGTGTTCCCTATGGAACCTATTGAAATATTT--	
11	gi 404561 S64539	----AGGAGATGGGGGTCACACTTAA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTGT	
12	gi 404561 S64539b	---TAGGAGATGGGGGTCACACTTAA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTG-	
13	gi 63712 X64710	--CTAGGAGATGGG---TCACATTTTATCTGTGTTCCCTATGGAACCTATTGAAATATTTG--	
14	gi 63712 X64710b	GACTAGGAGATGGG---TCACATTTTATCTGTGTTCCCTATGGAACCTATTGAAATAT----	
15	gi 64953 X56316	-ACTGCGAGATGGGG--TCACA--TATCTGTGTTCCCTATGGAACCTTTTTTTTTTTC--	
16		* ***** ** ***** ** * *	
17		NNNNNNNANATGGGNNNTACANNTANCTGTGTTCCCTATGGAACCTNNNTTNNNTNNNN	
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# Figure 107



# Figure 108



# Figure 109

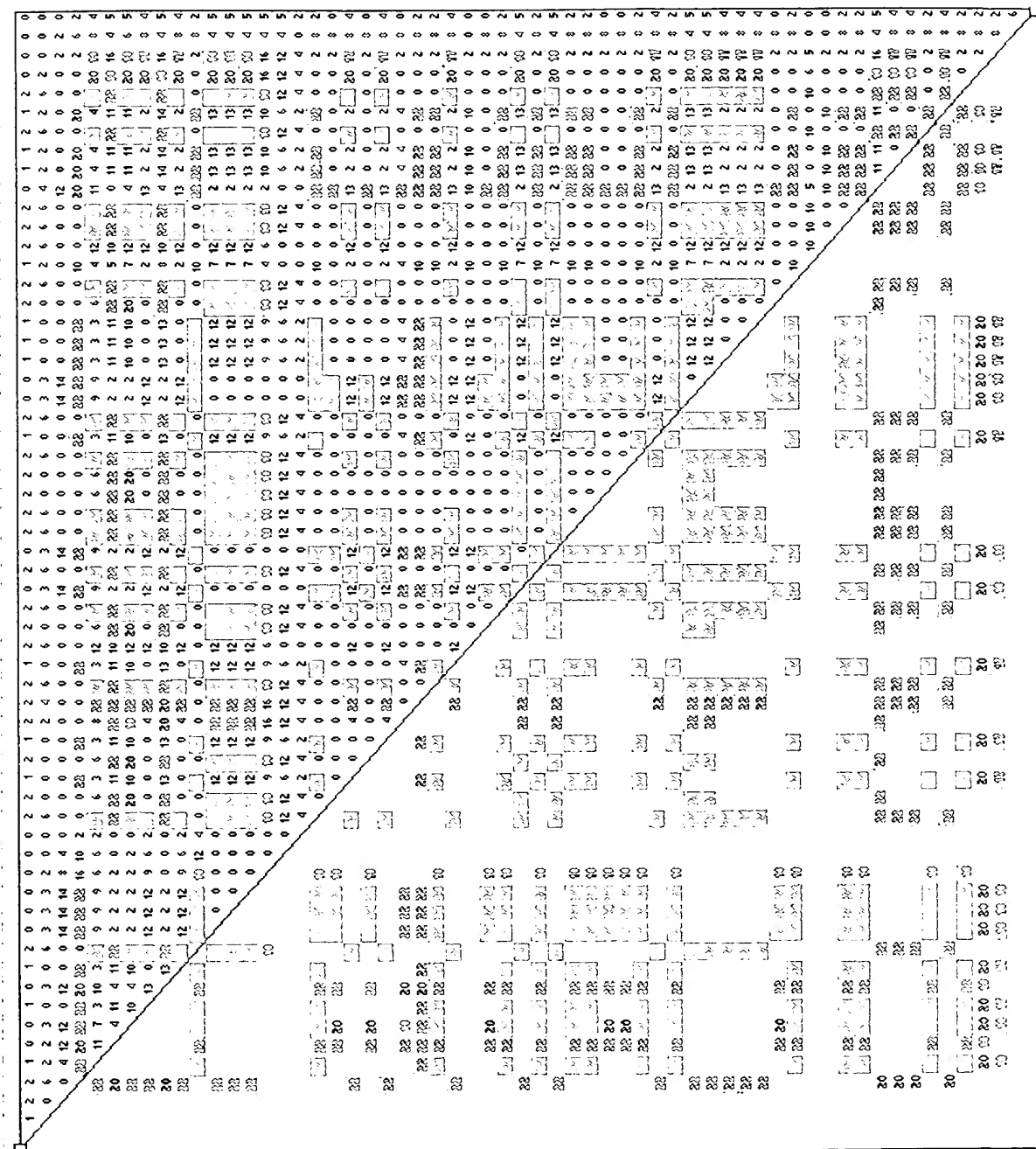
J:\cowxTargets\35135\seqs3p

Position:		Left Mean:	Left SD:	Right Mean:
Total hits:		Discarded:	Net:	Start:
Number	Description		Hits	
<input type="checkbox"/> 35135.fa	Homo sapiens 3 prime UTR ...			
<input checked="" type="checkbox"/> 64953.fa	Xenopus laevis 3 prime UTR...			
<input type="checkbox"/> 162173.fa	Trypanosoma brucei 3 prime...			
<input type="checkbox"/> 163448.fa	Bos taurus 3 prime UTR [ori...			
<input type="checkbox"/> 205807.fa	Rattus norvegicus 3 prime U...			
<input type="checkbox"/> 404561.fa	Mus musculus domesticus ...			
<input type="checkbox"/> 63712.fa	Gallus gallus 3 prime UTR [...			
<input type="checkbox"/> 200123.fa	Mus pahari 3 prime UTR [ori...			
<input type="checkbox"/> 2337849.fa	Ustilago maydis 3 prime UT...			

Region 1

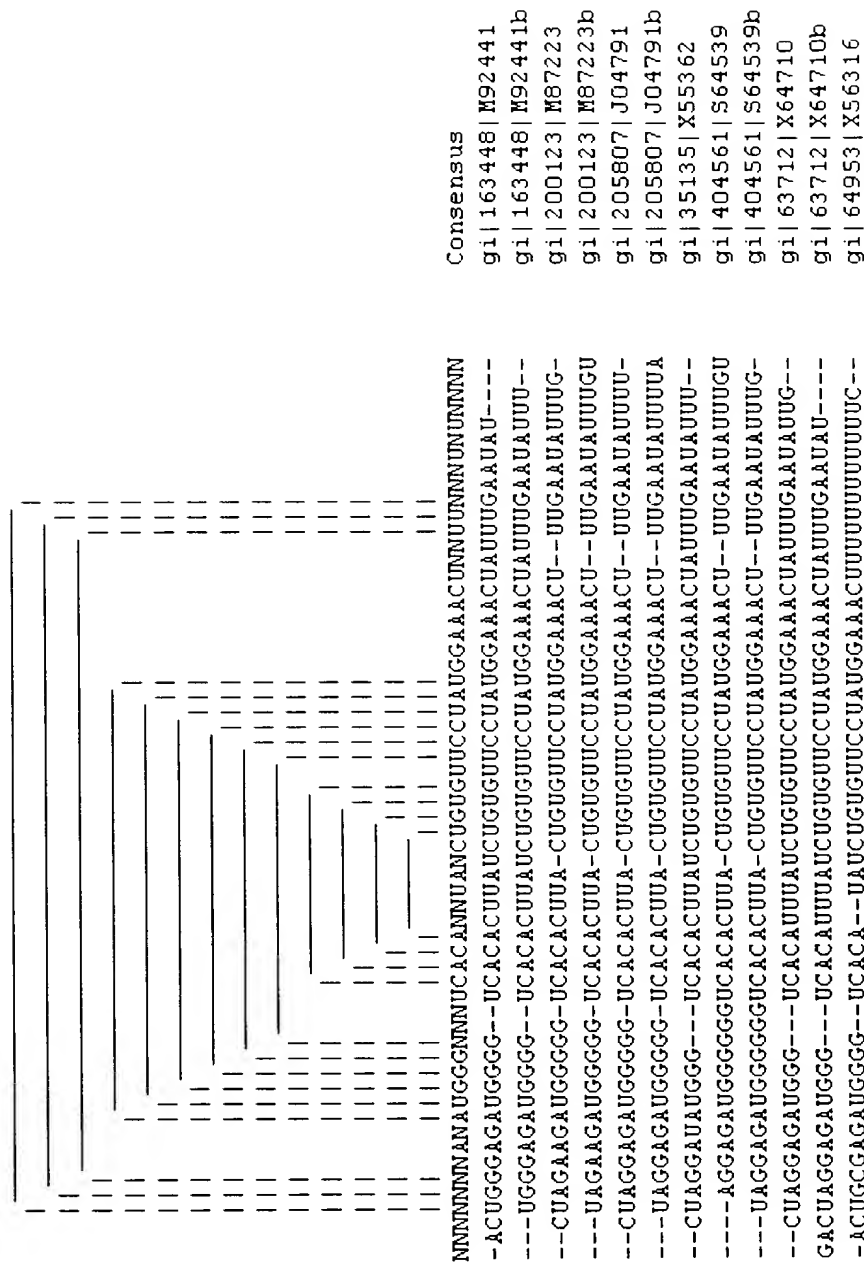
Region 2

Figure 110



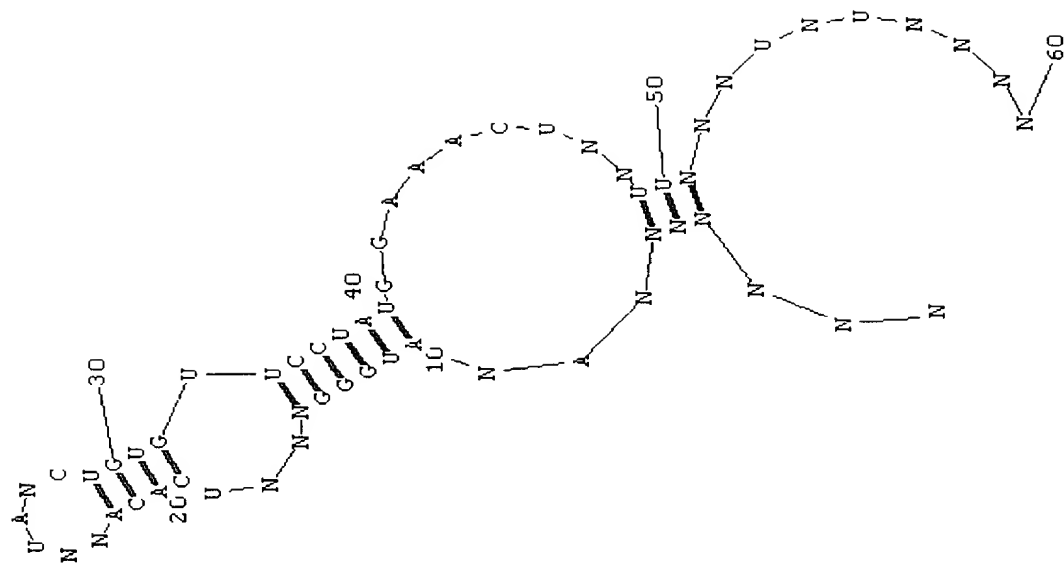
## Figure 111

Score: 300.0





**Figure 112**



## Figure 113

CLUSTAL W (1.74) multiple sequence alignment

```
gi|404561|S64539      CAAAGCGTTTGTAGCTTGT
gi|63712|X64710      CAAATATTGTAGCTTGT
gi|64953|X56316      CAAAGCATTGTAGCTTGT
gi|35135|X55362      CAAAGCATTGTAGCTTGT
gi|200123|M87223     CAAAGCATTATAGCTTGT
gi|205807|J04791     CAAAGCATTGTAGCTTGT
***** **
```

## Figure 114

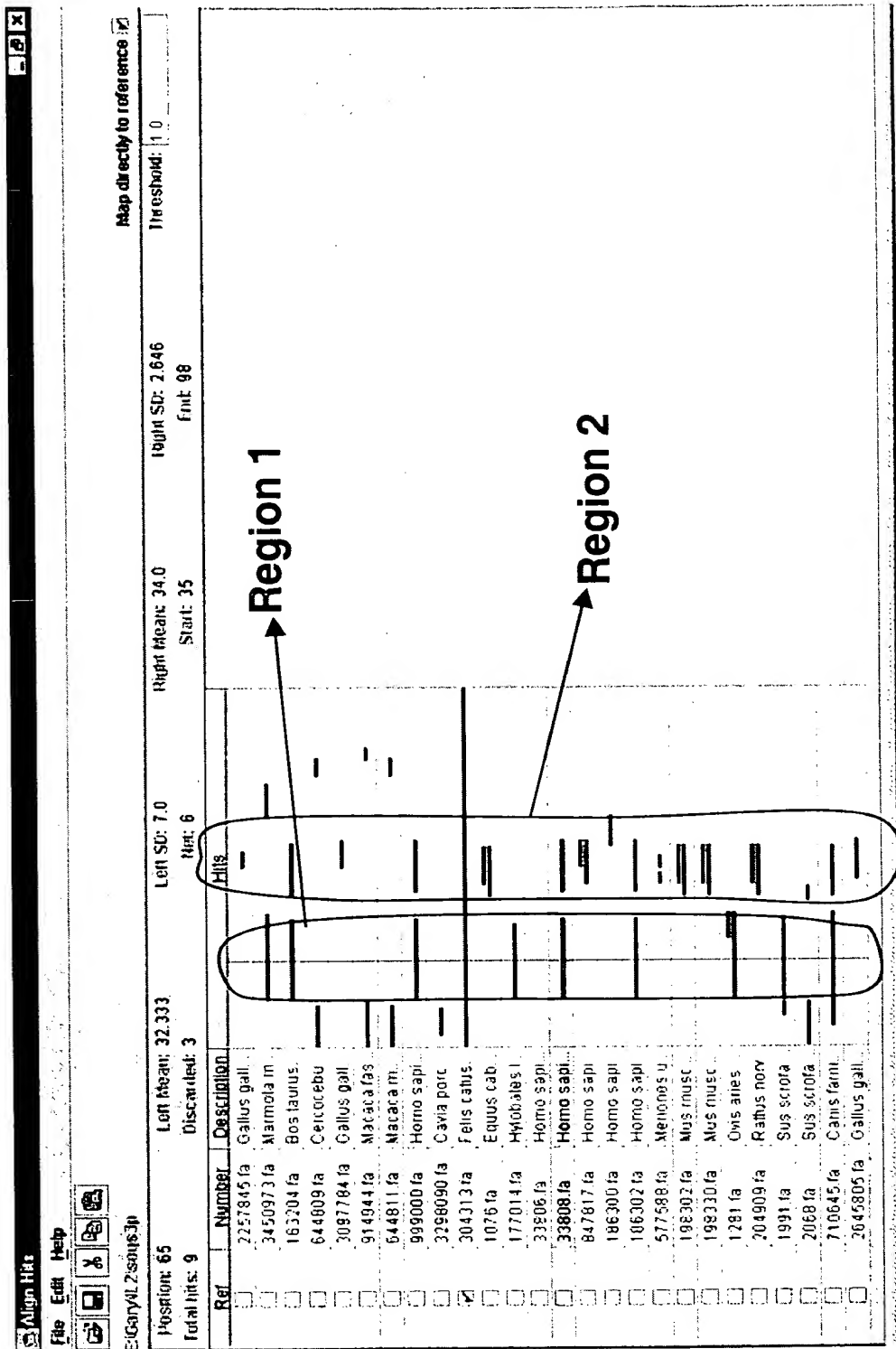
Score: 60.0

CAAGNNUUUNUAGCUUGU	Consensus
CAAGCGUUUGUAGCUUGU	gi 404561 S64539
CAAGUAAUUUGUAGCUUGU	gi 63712 X64710
CAAGCAUUUGUAGCUUGU	gi 64953 X56316
CAAGCAUUUGUAGCUUGU	gi 35135 X55362
CAAGCAUUUAUAGCUUGU	gi 200123 M87223
CAAGCAUUUGUAGCUUGU	gi 205807 J04791



[illegible]

# Figure 117



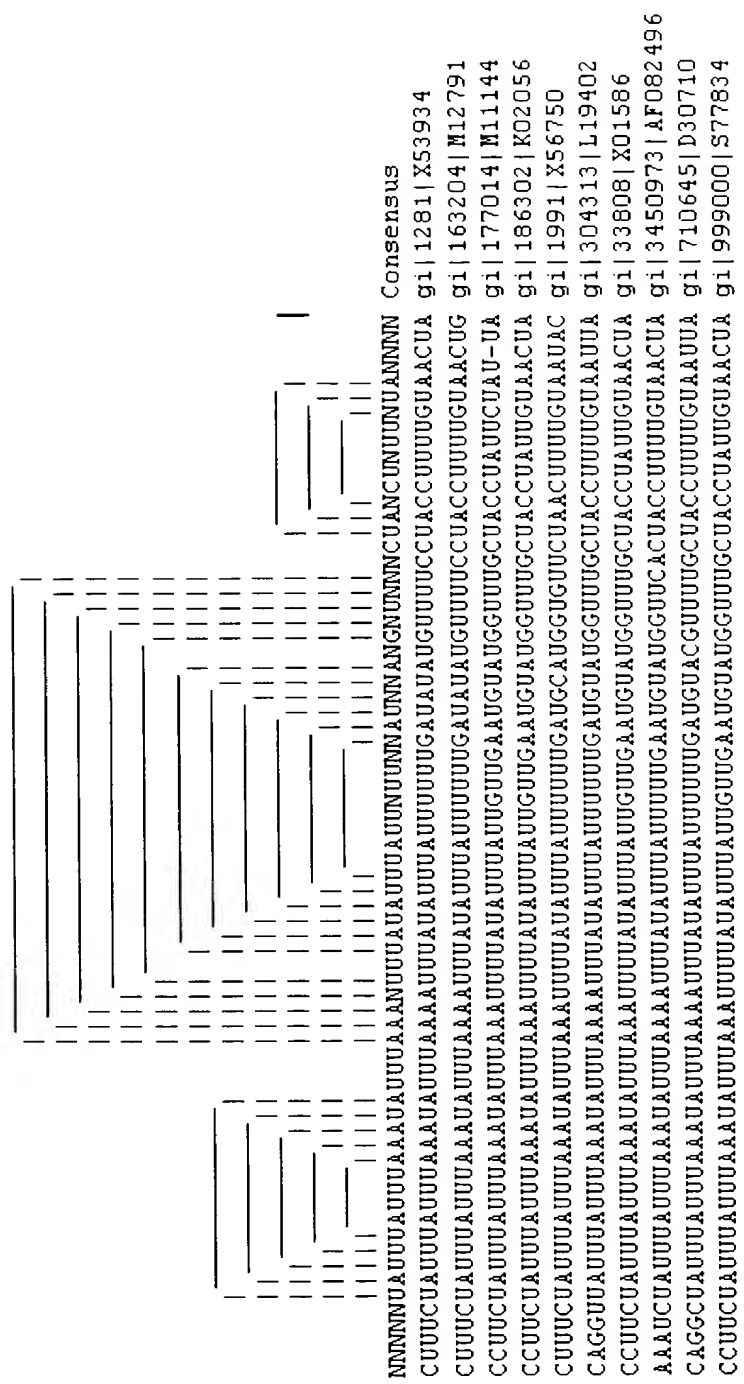
## Figure 118

CLUSTAL W (1.74) multiple sequence alignment

```
gi|1281|X53934      CTTTCTATTTTAAATATTTAAAAATTTTATATTTATTTTGTGATATATGTTTTCCTACCTTTTGTAACTA
gi|163204|M12791    CTTTCTATTTTAAATATTTAAAAATTTTATATTTTGTGATATATGTTTTCCTACCTTTTGTAACTG
gi|177014|M11144    CCTTCTATTTTAAATATTTAAAAATTTTATATTTATGTTGAATGATGGTTTGTCTACCTATTTCTAT-TA
gi|186302|K02056    CCTTCTATTTTAAATATTTAAAAATTTTATATTTATTTGTTGAATGATATGGTTTGTCTACCTATTTGTAACTA
gi|1991|X56750      CTTTCTATTTTAAATATTTAAAAATTTTATATTTTGTATGCAATGGTGTCTAACTTTTGTAAATAC
gi|304313|L19402    CAGGTTATTTTAAATATTTAAAAATTTTATATTTTGTATGATGGTTTGTCTACCTTTTGTAAATTA
gi|33808|X01586     CCTTCTATTTTAAATATTTAAAAATTTTATATTTATGTTGAATGATGGTTTGTCTACCTATTTGTAACTA
gi|3450973|AF082496 AATCTATTTTAAATATTTAAAAATTTTATATTTATTTTGAATGATATGGTTTGTCTACCTTTTGTAACTA
gi|710645|D30710    CAGGCTATTTTAAATATTTAAAAATTTTATATTTTGTATGATCGTTTGTCTACCTTTTGTAAATTA
gi|999000|S77834    CCTTCTATTTTAAATATTTAAAAATTTTATATTTATGTTGAATGATATGGTTTGTCTACCTATTTGTAACTA
```

Figure 119

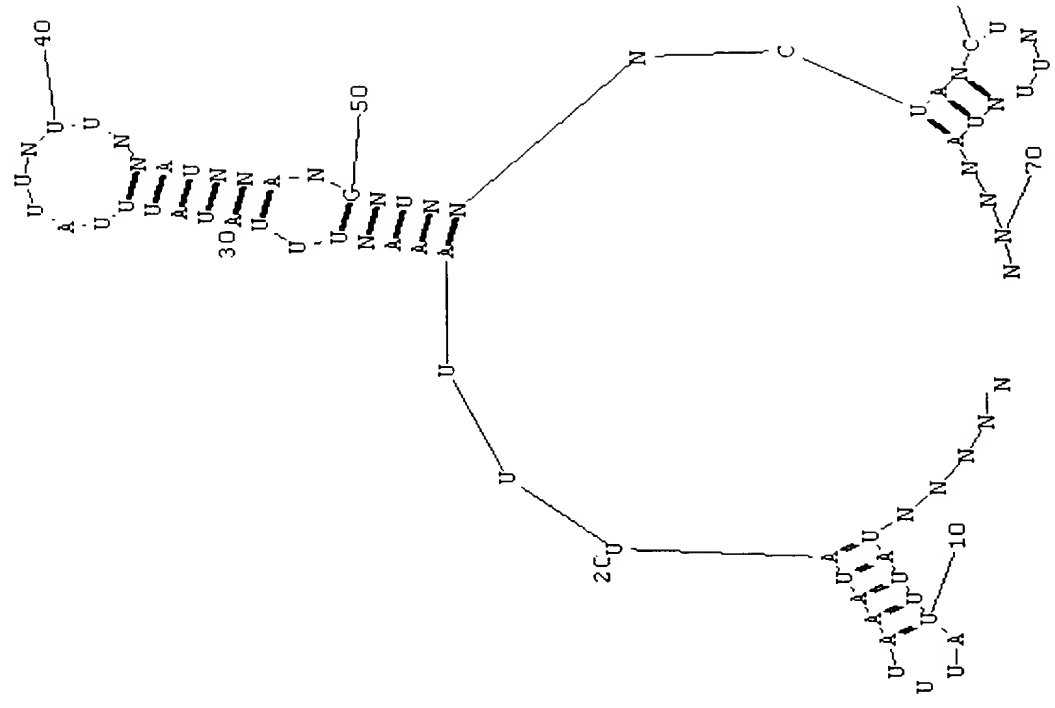
Score: 404.0





100% pure and free of any other substances. The product is a white, crystalline solid.

Figure 120



# Figure 121

CLUSTAL W (1.74) multiple sequence alignment

g1 1076 X69393	TGATAAATATG--GATCTTTTAAGATTCTTTTGTAG-CCCCXXXXXX-
g1 163204 M12791	TGATAAATATG--GATCTTTTAAGATTCTTTTGTAG-CCCTACGGGC-
g1 186300 M22005	XXXXXXXXXX--XXXXXXXXXXXXXXXXXXXXXXTCCACCCCTGA--
g1 186302 K02056	CTATAAATATG--GATCTTTTATGATTCCTTTTGTAG-CCCTACGGGC-
g1 198302 K02797	TGATAAATATG--GATCTTTAAAGATTCTTTTGTAGCCCCCAAGGC--
g1 198330 K02292	TGATAAATATG--GATCTTTAAAGATTCTTTTGTAGCCCCCAAGGC--
g1 204909 M22899	TGATAAATATG--GATCTTTAAAGATTCTTTTGTAGCCCCCAAGGC--
g1 2068 X58428	TGATAAATGATCAGCGCXXXXXXXXXXXXXXXXXX-XXXXXX----
g1 2257845 AF000631	-CTCTCTTCTAA-GATCATATTTGATCCTTTCTGTAA--CCTACGGGCTC
g1 2645805 AF033563	-CTCTCTTCTAA-GATCATATTTGATCCTTTCTGTAGCCCTACGGGC--
g1 304313 L19402	TGATAAACATG--GATCTTTTAAAGATTCTTTTGTAG-CCCTACGGGT-
g1 3087784 AJ224516	-CTCTCTTCTAA-GATCATATTTGATCCTTTCTGTAGCCCTACGGGC--
g1 33808 X01586	CTATAAATATG--GATCTTTTATGATTCCTTTTGTAG-CCCTACGGGC-
g1 577588 X68779	CGATAAATATG--GATCTTTAGAGATTCTTTTGTAG--CCCAAGGGCTC
g1 710645 D30710	TGATAAATATG--GATCTTTTAAAGATTCTTTTGTAG-CCCCXXXXXX-
g1 847817 U25676	CTATAAATATG--GATCTTTTATGATTCCTTTTGTAG-CCCTACGGGC-
g1 999000 S77834	CTATAAATATG--GATCTTTTATGATTCCTTTTGTAG-CCCTACGGGC-

## Figure 122

Score: 412.0

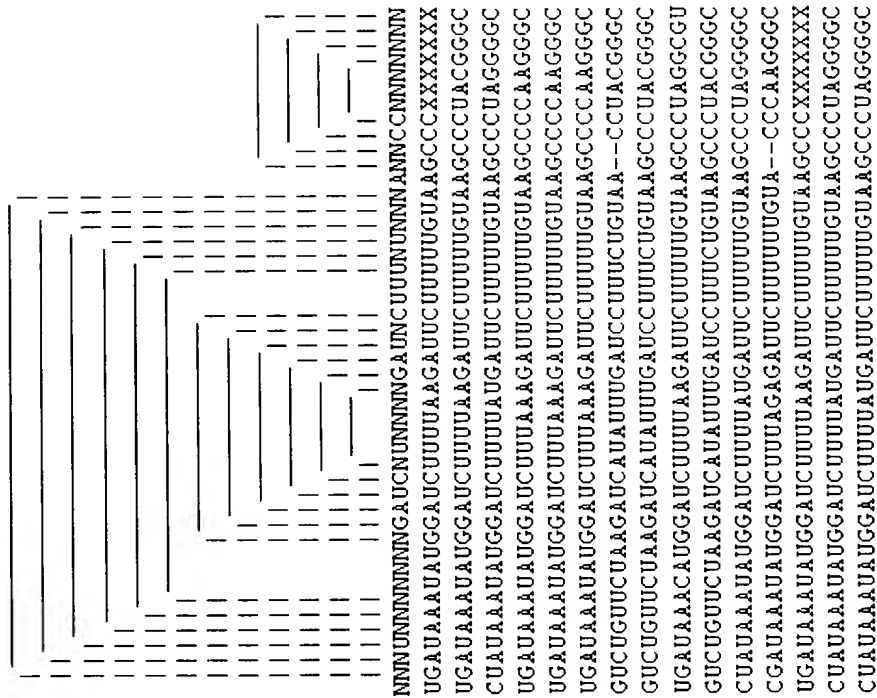
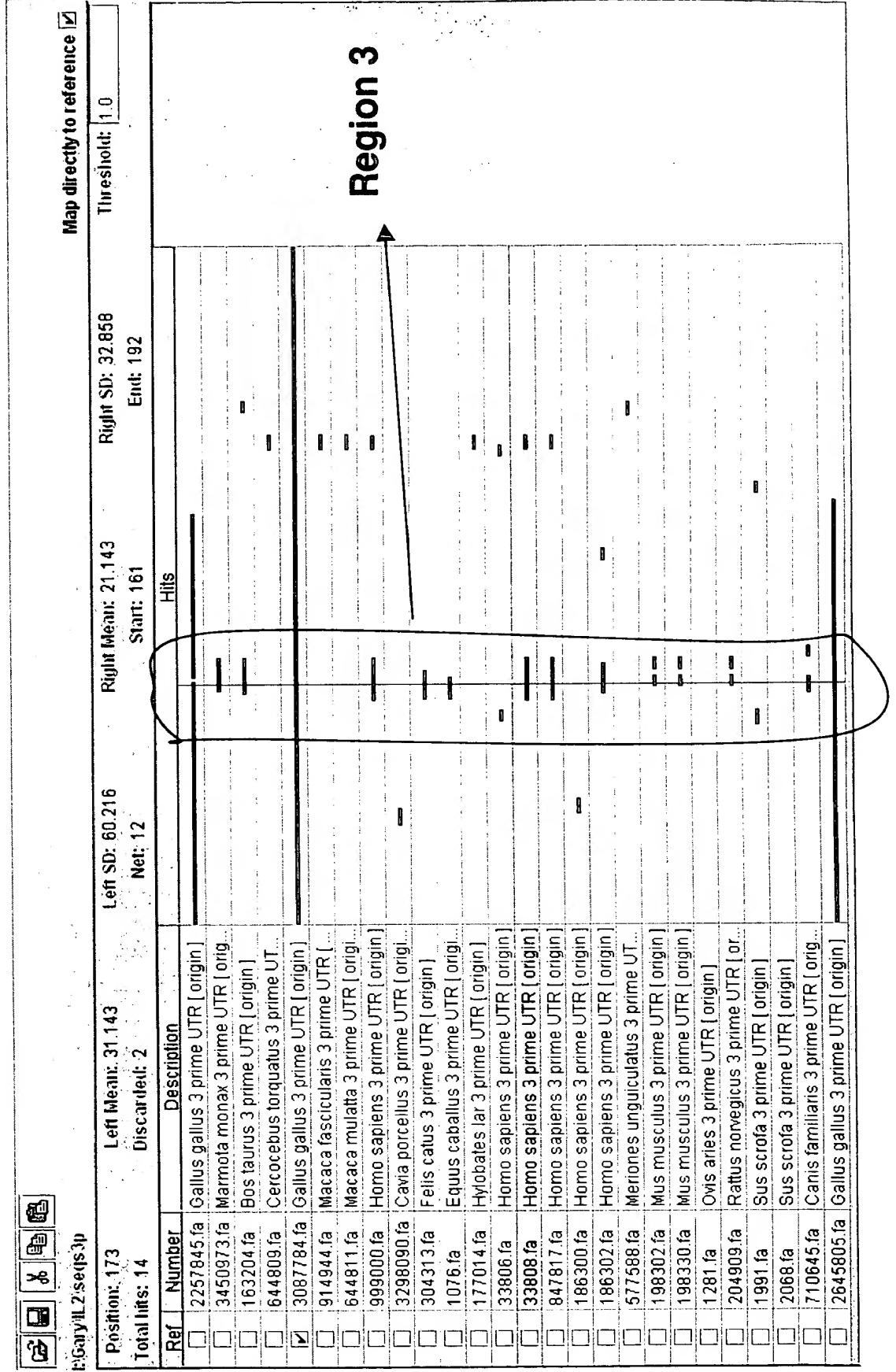




Figure 124



# Figure 125

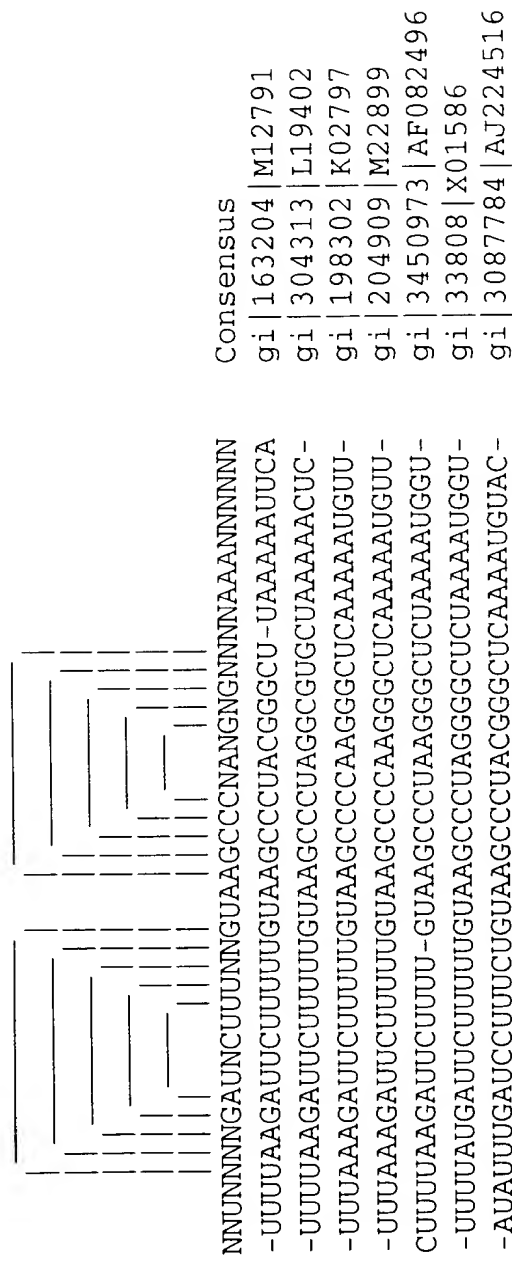
CLUSTAL W (1.74) multiple sequence alignment

gi 163204 M12791	-TTTAAAGATTCTTTTGTAAAGCCCTACGGGCT-TAAAAATTCA
gi 304313 L19402	-TTTAAAGATTCTTTTGTAAAGCCCTAGGCGTGCTAAAAACTC-
gi 198302 K02797	-TTTAAAGATTCTTTTGTAAAGCCCCCAAGGGCTCAAAAAATGTT-
gi 204909 M22899	-TTTAAAGATTCTTTTGTAAAGCCCCCAAGGGCTCAAAAAATGTT-
gi 3450973 AF082496	CTTTAAAGATTCTTTT-GTAAGCCCTAAGGGCTCTAAAAATGGT-
gi 33808 X01586	-TTTATGATCTTTTGTAAAGCCCTAGGGGCTCTAAAAATGGT-
gi 3087784 AJ224516	-ATATTGATCCTTTCTGTAAAGCCCTACGGGCTCAAAAAATGTAC-

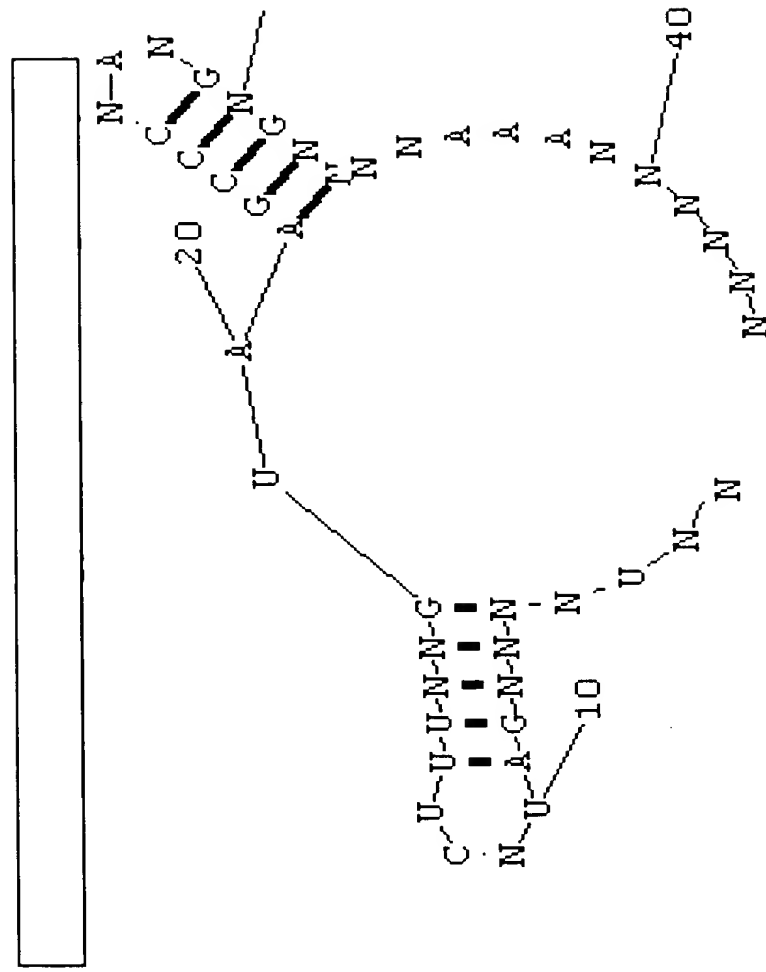
\*   \*   \*   \*   \*   \*   \*   \*   \*   \*   \*   \*

## Figure 126

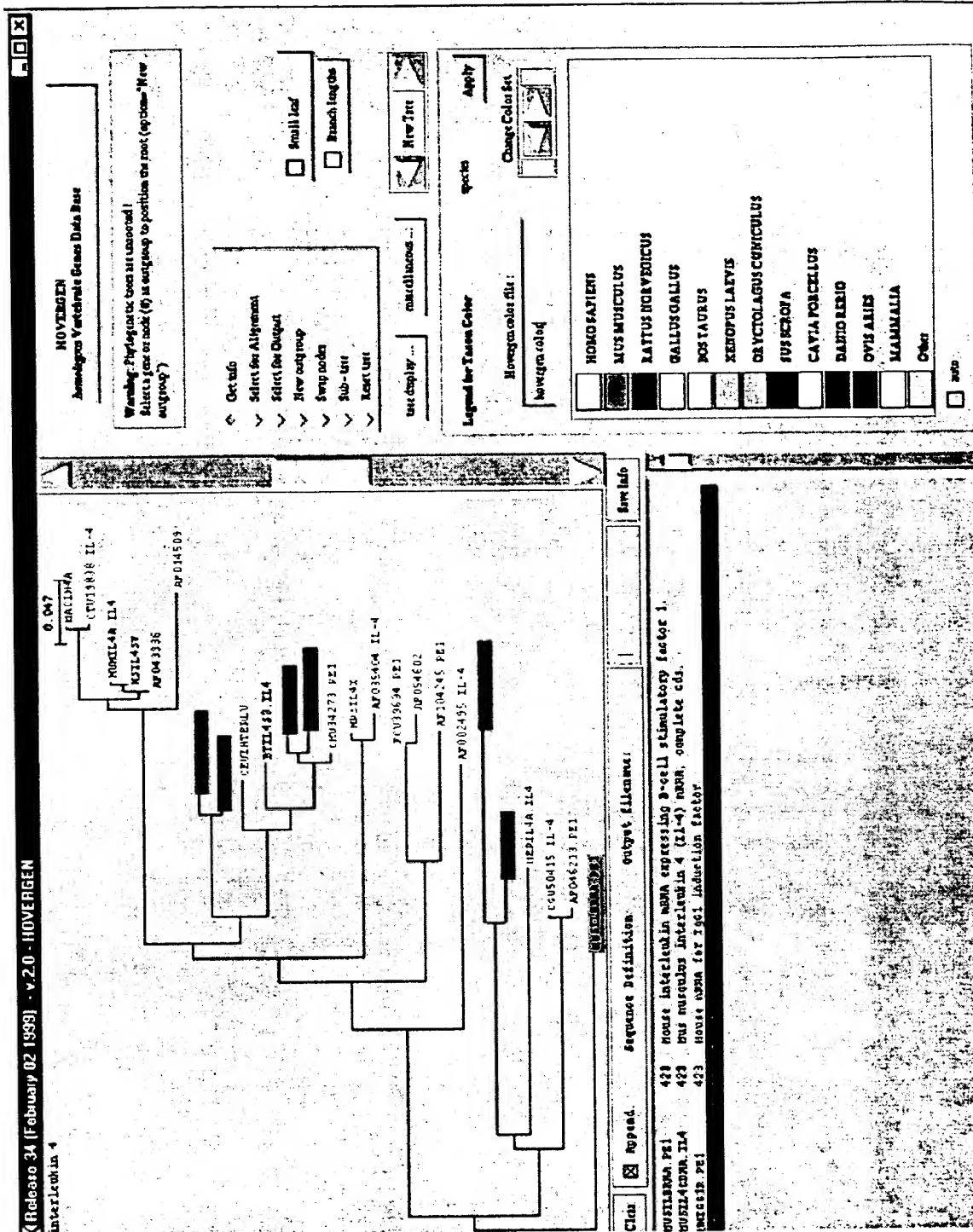
Score: 165.0



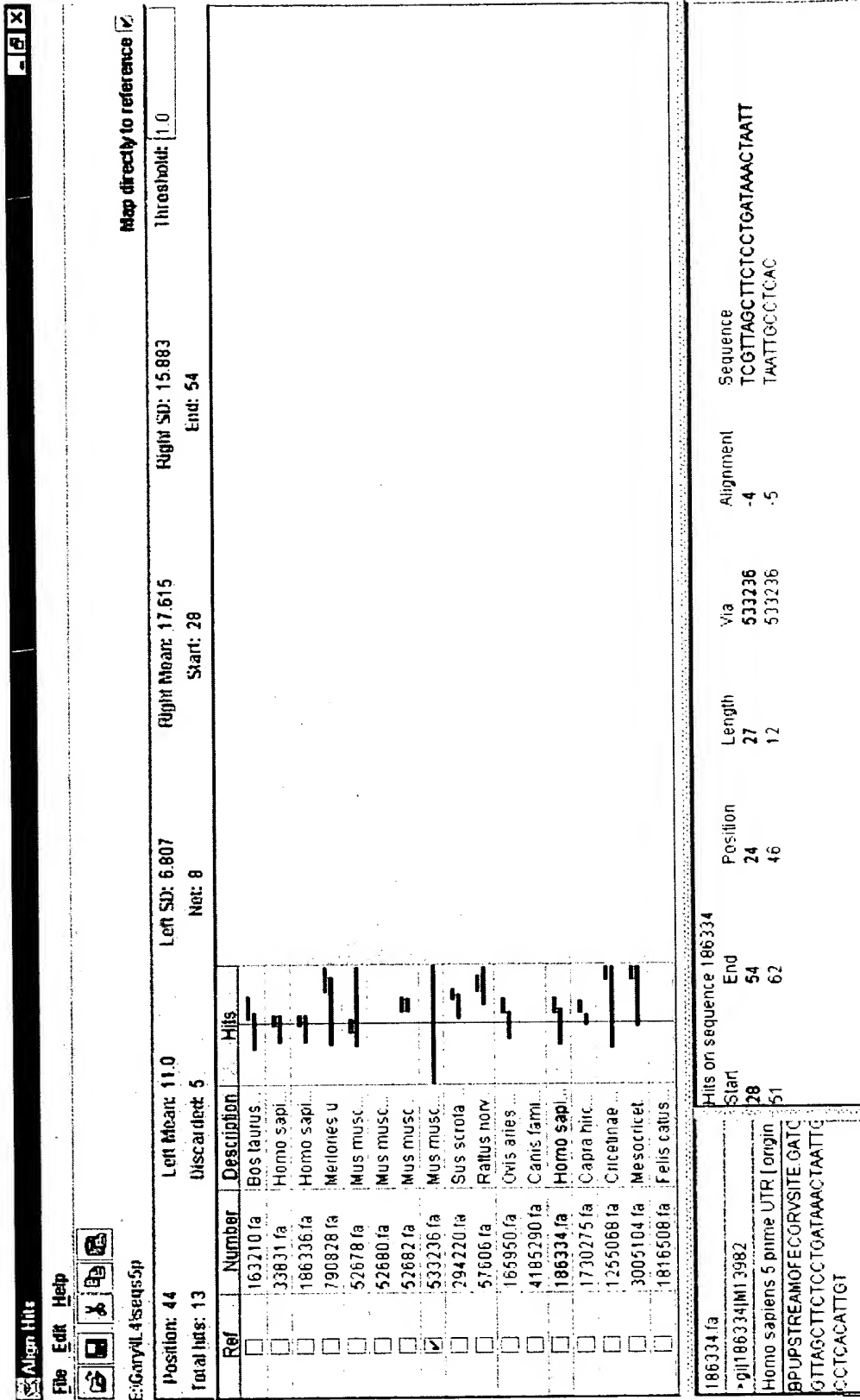
## Figure 127





[illegible]

# Figure 129



# Figure 130

CLUSTAL W (1.74) multiple sequence alignment

gi 1255068 U50415	XXXTGCA TTGTTAGCGTCTCTTGATAACCTTAAT-TGTCCTCTATCACTGA---
gi 163210 M77120	-XXXXTGCATTGTTAGCGTCTCTCTGGTAAACTAAATTGTCTCACATTGTCTAGT--
gi 165950 M96845	-XXXXXXXXXXXTAGCTTCTCCTGATAATCTAATTGCCCTCACACTGTCAGT--
gi 1730275 U34273	-XXXXXXXXXXXTAGCTTCTCCTGATAAACTAAATTGTCTCACACTGTCAGT--
gi 186334 M13982	-----GATCGTTAGCTTCTCCTGATAAACTAAATTGCCCTCACATTGTGTXXX---
gi 186336 M23442	-GCATTGCATCGTTAGCTTCTCCTGATAAACTAAATTGCCCTCACATTGTCTACT--
gi 294220 L12991	---XXXXXXXXXXXXXXXXXXGGTAAACTAAATTGTCTCACATCGTCAGTGC
gi 3005104 AF046213	XXXXXXXXXXXXXXXXXXXXTTGATAACCTTAAATTGTCTCTATCACTGA---
gi 33831 X06750	-GCATTGCATCGTTAGCTTCTCCTGATAAACTAAATTGCCCTCACATTGTCTACT--
gi 52678 X05064	GCATTGCATTGTTAGCATCTCTTTGATAAACTTAAATTGTCTCTCGTCACTGA---
gi 52678 X05064b	-GTGTGCGCAAGGCAGACTTCTTTGATA-TTACTCTGTCTTTCCCCAGGGCGA-
gi 52682 X05253	XXXXXXXXXXCCCGCCGACAGCGAGACCCAAATCTGTCTCACAAATGA AAC---
gi 533236 M25892	GGGGGGATTGTTAGCATCTCTTTGATAAACTTAAATTGTCTCTCGTCACTGA---
gi 790828 L37779	XXXXXXXXATTGTTGGCATCTCTTTGACAAACTTAAATTGTCTCACATCCCTGA---

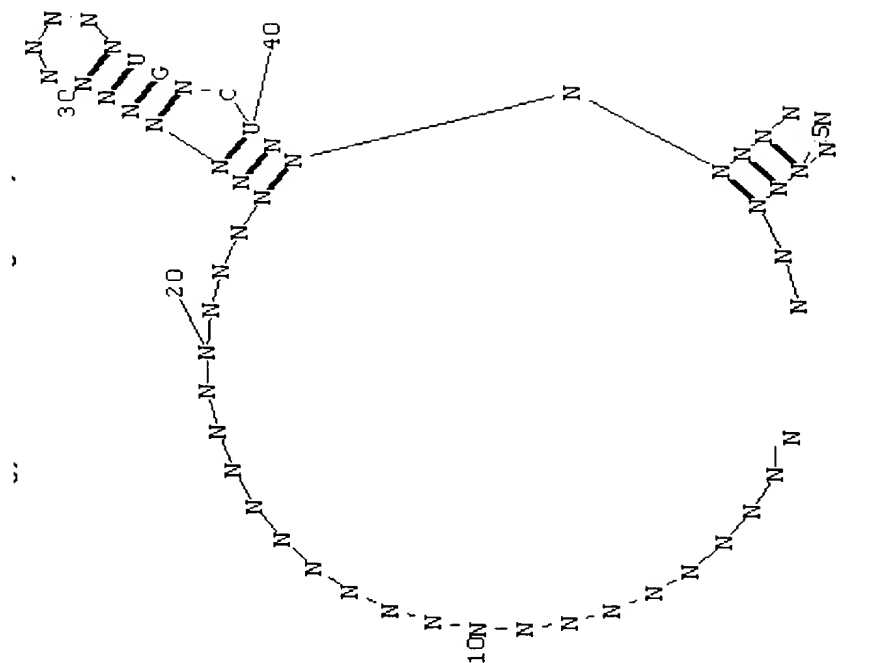
[illegible]

## Consensus

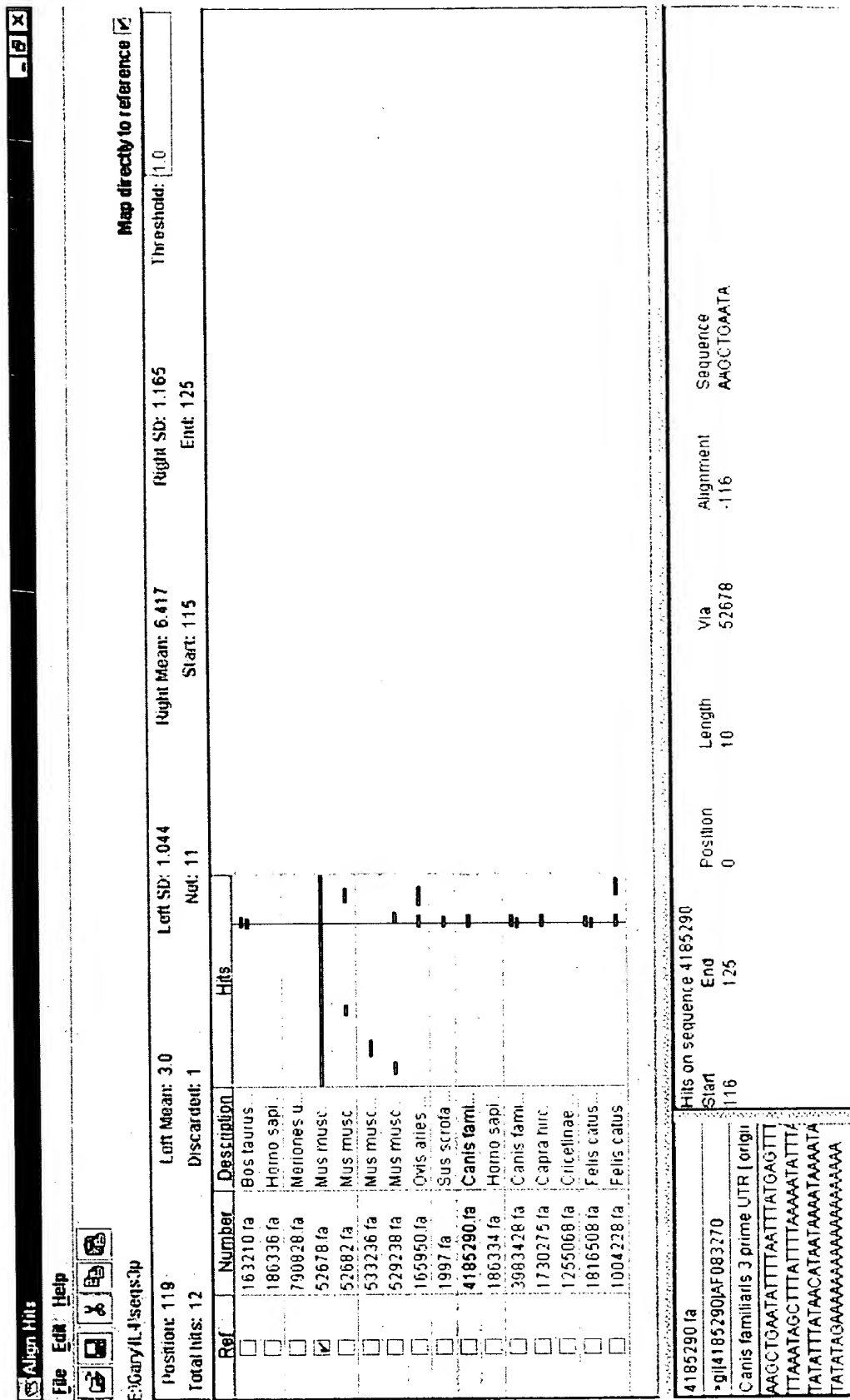
gi|1255068|U50415  
gi|163210|M77120  
gi|165950|M96845  
gi|1730275|U34273  
gi|186334|M13982  
gi|186336|M23442  
gi|294220|L12991  
gi|3005104|AF046213  
gi|33831|X06750  
gi|52678|X05064  
gi|52678|X05064b  
gi|52682|X05253  
gi|533236|M25892  
gi|790828|L37779

Figure 131

Figure 132



# Figure 133



## Figure 134

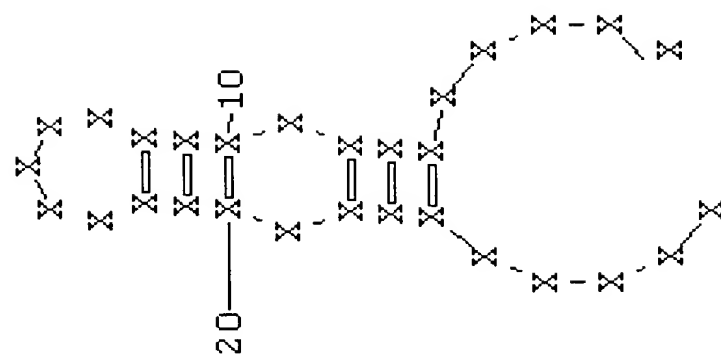
CLUSTAL W (1.74) multiple sequence alignment

```
gi|1004228|X87408      TTATAATTATTATATAAATAAGTATATGT-
gi|1004228|X87408b    XXXXXAAGCTGAATATCTTAATTTATGAG
gi|163210|W77120      ATGTAGAGCTGAAAAAAXXXXXXXX
gi|163210|W77120b    XXXXXAAGCTGAATATTTTAAATTTATGAG
gi|165950|W96845      AATTTATGCTTTTAAATAGCTTATAT---
gi|165950|W96845b    XXXXXAAGCTGAATATTTTAAATTTATGAC
gi|1730275|U34273     XXXXXAAGCTGAATATTTTAAATTTATGAC
gi|1816508|U39634     ATGTAGAACTGAAAAAATAAATAAATAA
gi|1816508|U39634b   XXXXXAAGCTGAATATCTTAAATTTATGAG
gi|1997|X68330        XXXXXAAGCTGACTATTTTAAATTTATGAT
gi|3983428|AF104245   ATATAGACCCTAAAAAATAAATAAATAA
gi|3983428|AF104245b XXXXXAAGCTGAATATTTTAAATTTATGAG
gi|4185290|AF083270   XXXXXAAGCTGAATATTTTAAATTTATGAG
gi|52678|X05064       ACACGAATCTGAATGAGAAATGCCTGTGAT
gi|52682|X05253       ACTTCATTGCCATAAGGTTCTACTGTTAG
gi|529238|L32955      ATAAAAACAACAACCTTCCTCCXXXXXXX
gi|529238|L32955b    GTGTCCCACTGAAGGAGCAAGGCTCAGGC
```

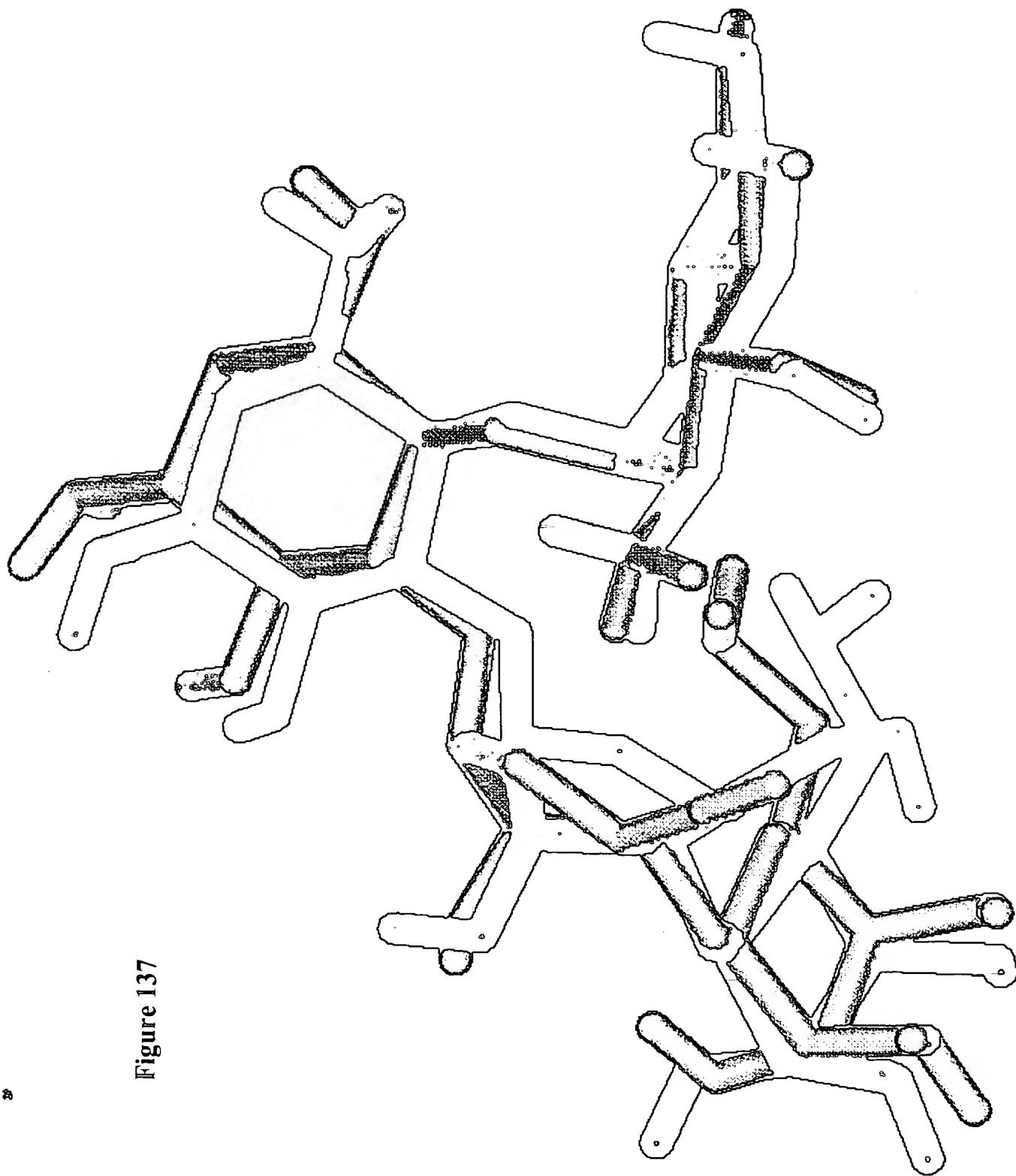




Figure 136



**Figure 137**



bioRxiv preprint doi: <https://doi.org/10.1101/111111>; this version posted January 1, 2018. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Energy score vs. RMSD

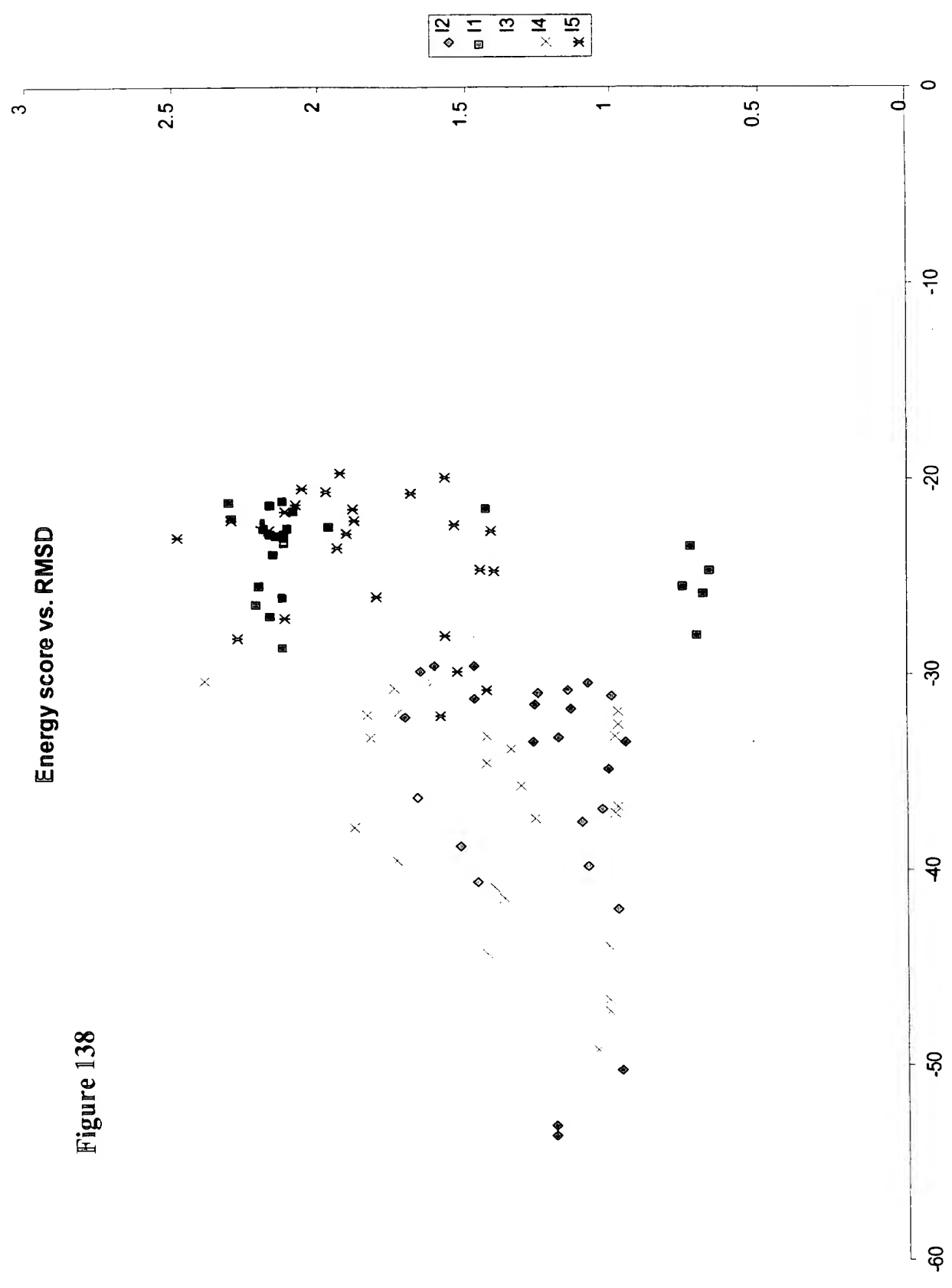


Figure 139

# MASS of 60-Member Ibis Library Against 16S A-site RNA

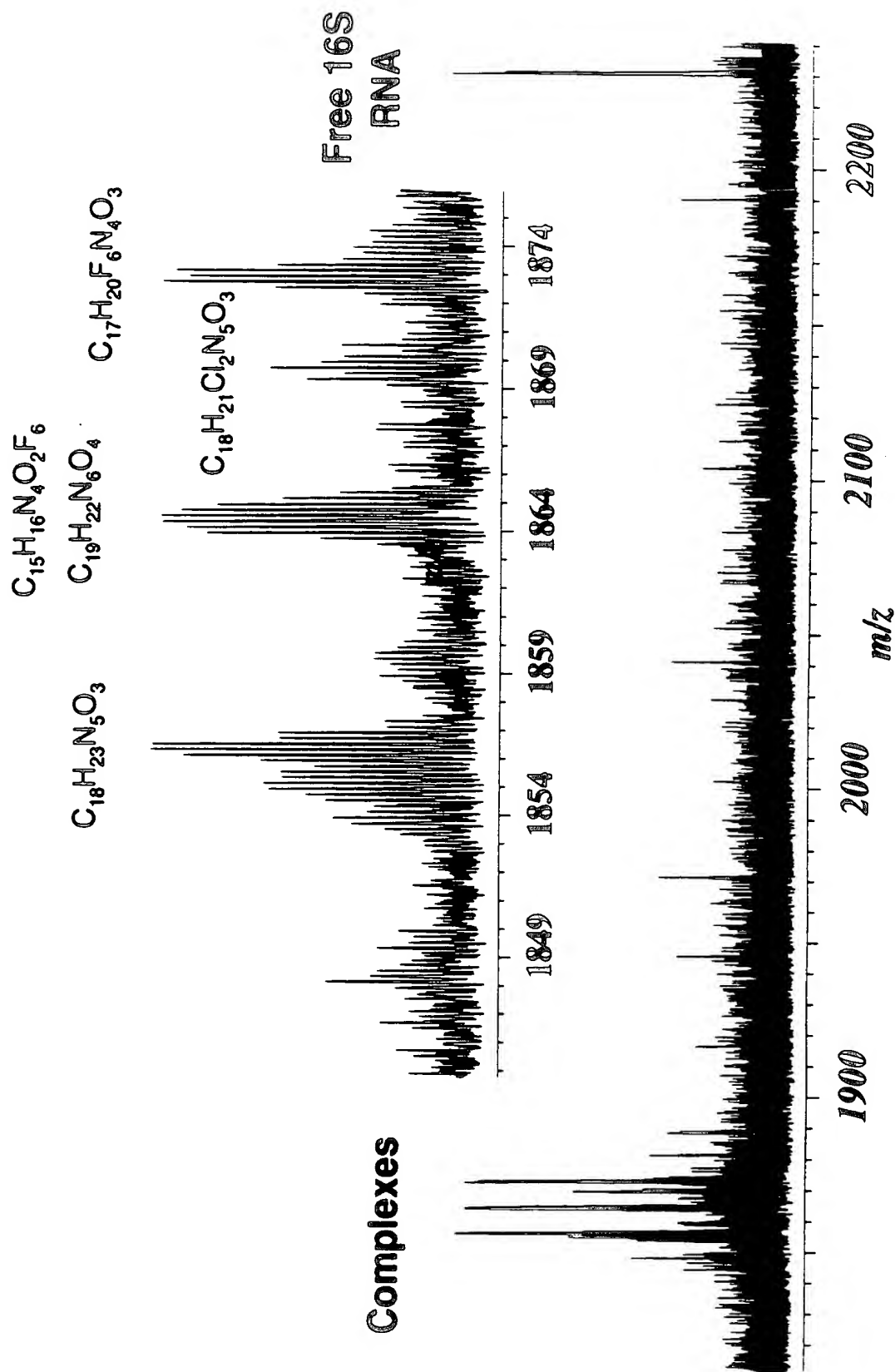


Figure 140

# MASS of 60-member Library against 16S A-site Model

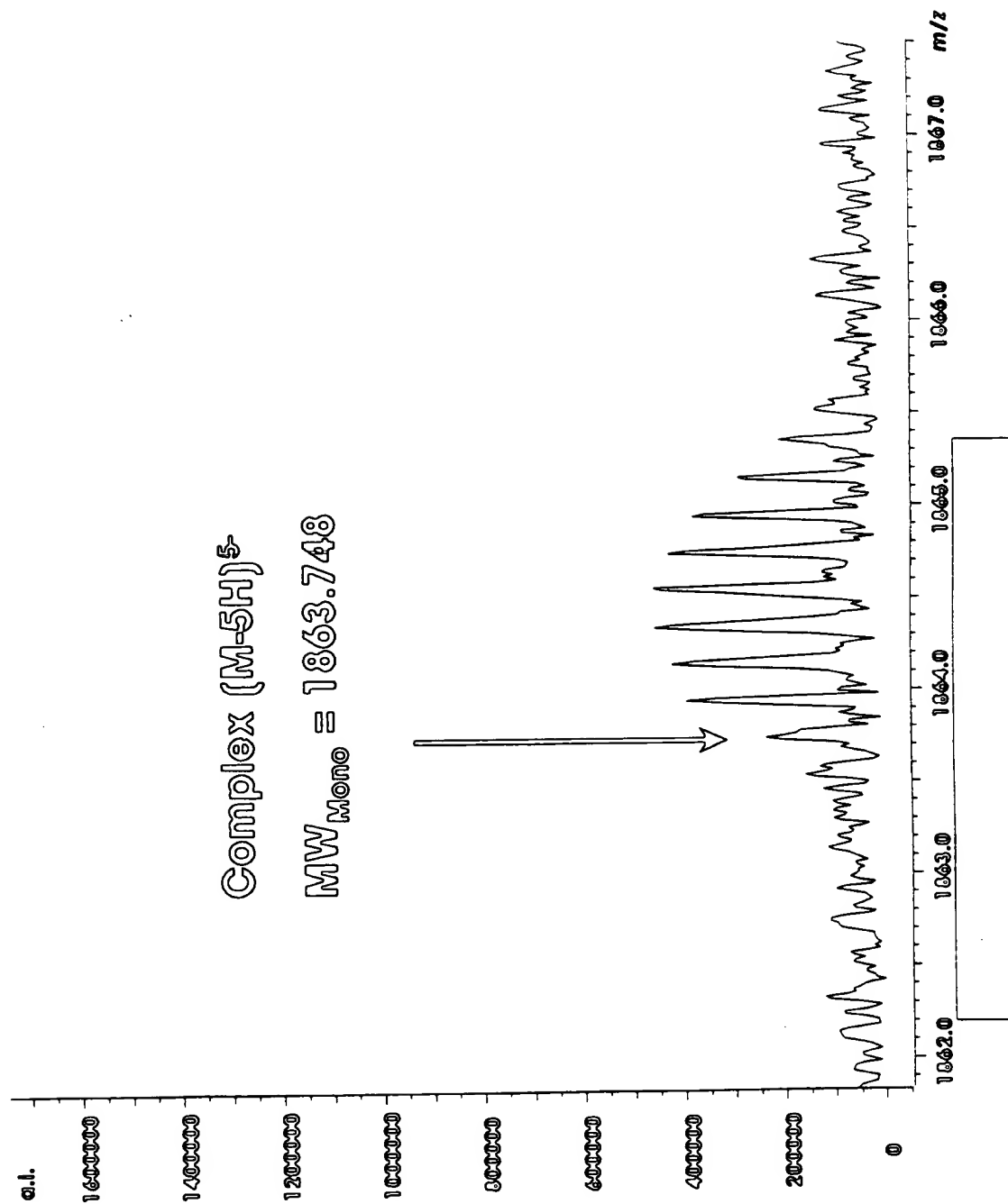


Figure 141

# FT-ICR MS of Starting Library

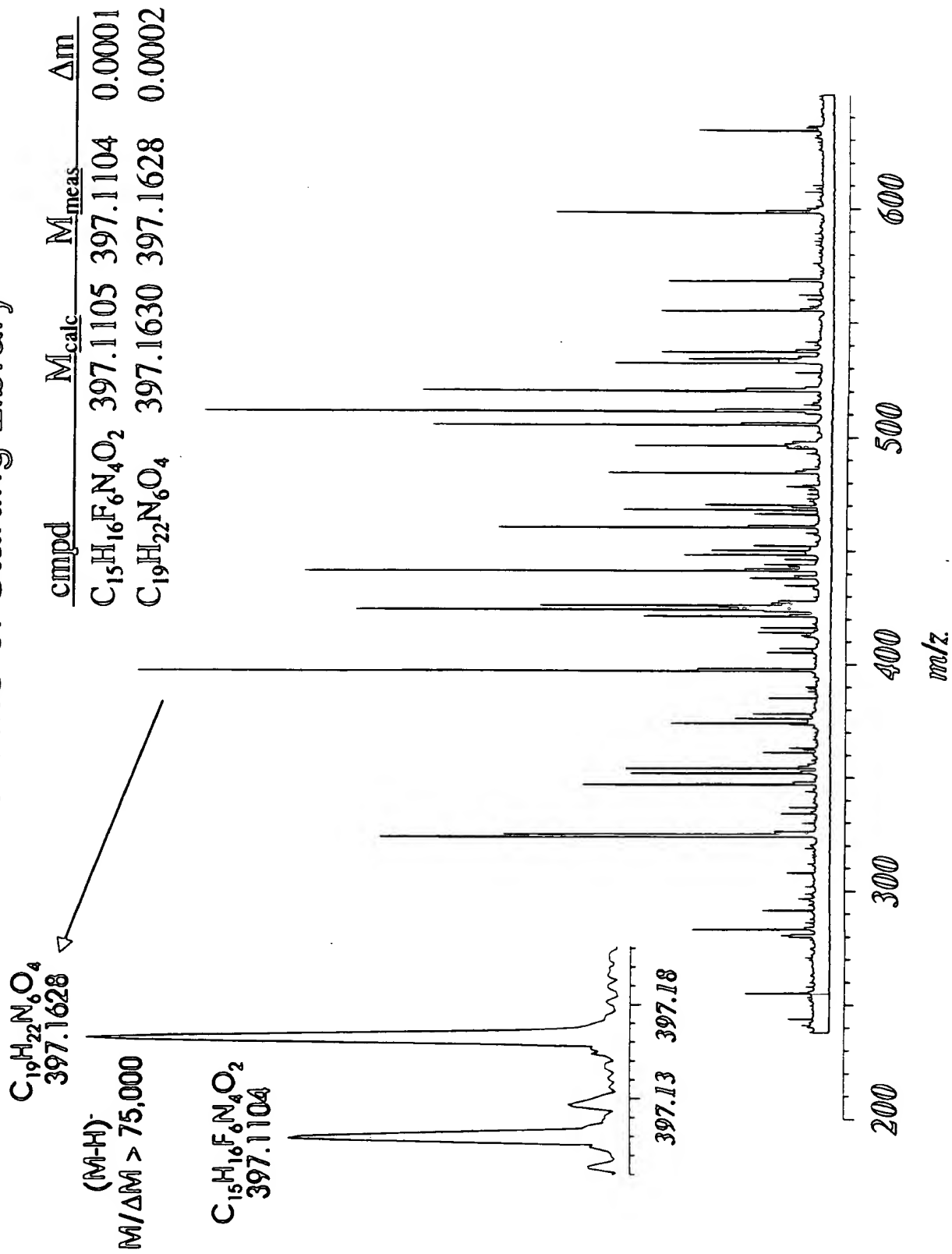


Figure 142

# Compound Identification from a 60-member Combinatorial library with MASS

Complex $M_{meas}$	9320.300 $\pm$ .009 Da
RNA $M_{meas}$	8922.189 $\pm$ .009
$\Delta M$	398.111 $\pm$ .009 Da

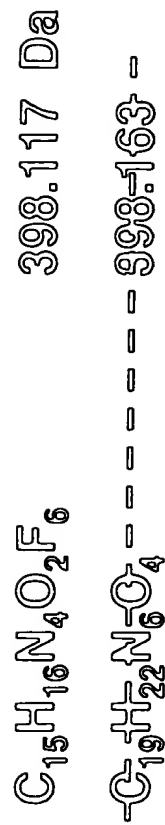


Figure 143

# Elemental Composition Constraints

Measured Mass: 615.2969

Mass Tolerance: 1.0 ppm

Charge: 0

Element Min. atoms Max. atoms

<sup>12</sup> C	12	30
<sup>1</sup> H	23	60
<sup>16</sup> O	7	20
<sup>14</sup> N	3	20

Possible Elemental Compositions:

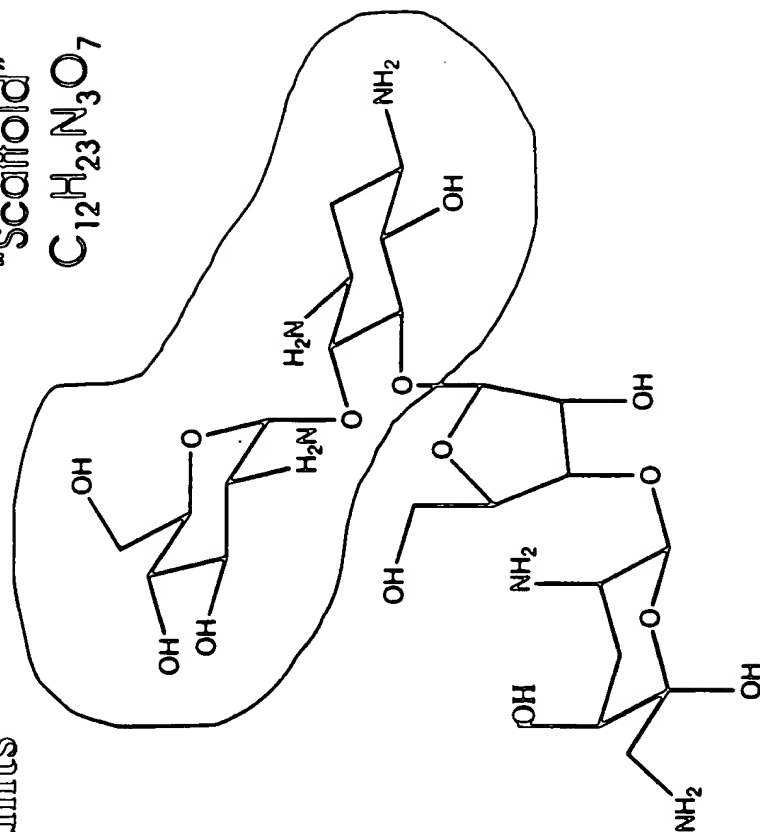
Calc. Mass Error Molecular Formula

(amu) (ppm)

615.296291	-0.98	<sup>16</sup> O <sub>4</sub> <sup>14</sup> N <sub>19</sub> <sup>12</sup> C <sub>21</sub> <sup>1</sup> H <sub>33</sub>
615.296298	0.98	<sup>16</sup> O <sub>9</sub> <sup>14</sup> N <sub>12</sub> <sup>12</sup> C <sub>22</sub> <sup>1</sup> H <sub>39</sub>
615.296305	0.97	<sup>16</sup> O <sub>14</sub> <sup>14</sup> N <sub>5</sub> <sup>12</sup> C <sub>23</sub> <sup>1</sup> H <sub>45</sub>
-615.296808	-0.15	<sup>16</sup> O <sub>15</sub> <sup>14</sup> N <sub>17</sub> <sup>12</sup> C <sub>8</sub> <sup>1</sup> H <sub>41</sub>
-615.296815	-0.14	<sup>16</sup> O <sub>20</sub> <sup>14</sup> N <sub>10</sub> <sup>12</sup> C <sub>9</sub> <sup>1</sup> H <sub>47</sub>

Further constrain by elemental composition of "letters" unintended products...

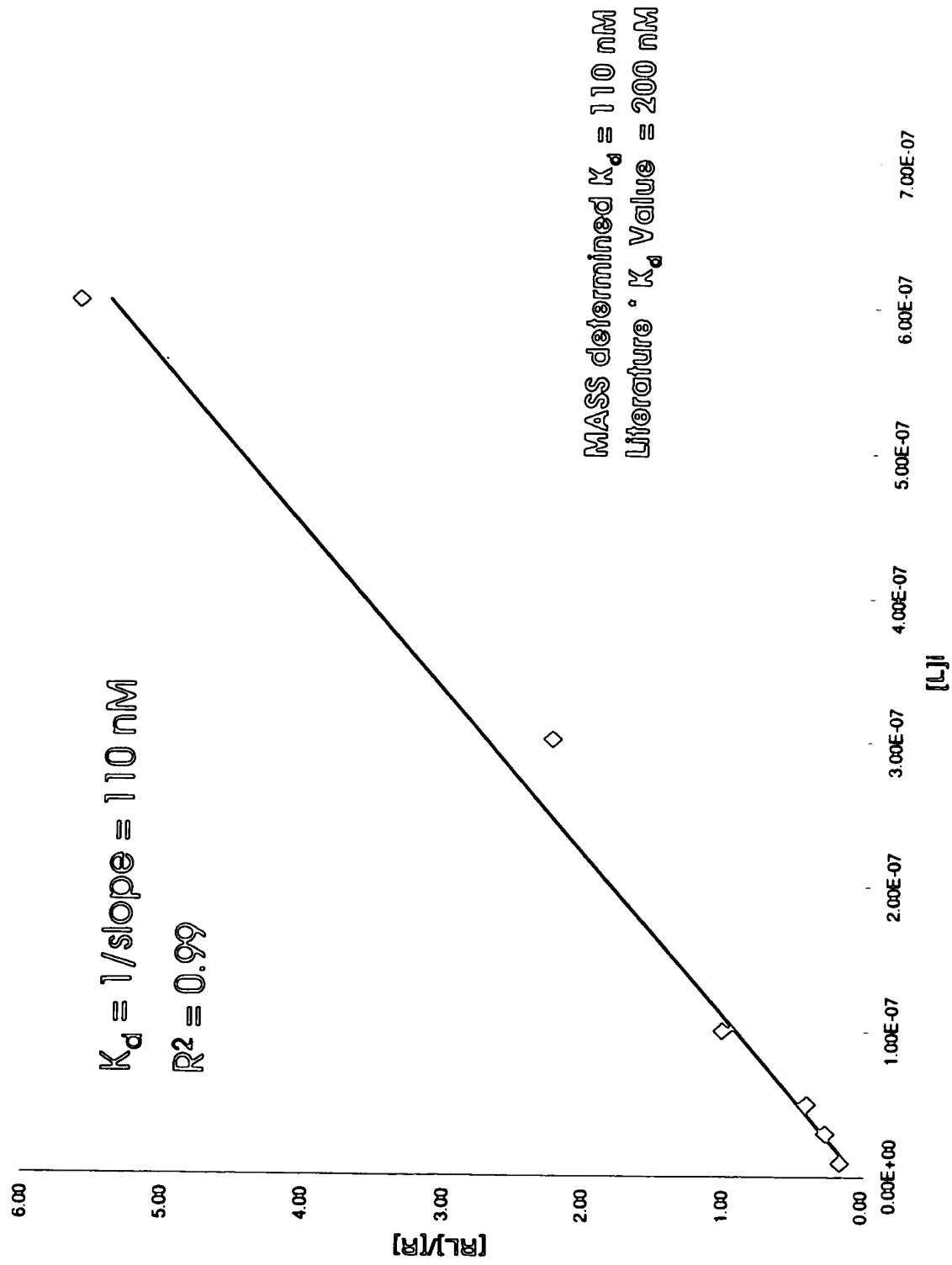
"Scaffold"  
C<sub>12</sub>H<sub>23</sub>N<sub>3</sub>O<sub>7</sub>





# MASS $K_d$ determination for 16S-Paromomycin

Figure 144



# Multitarget Affinity/Specificity Screening

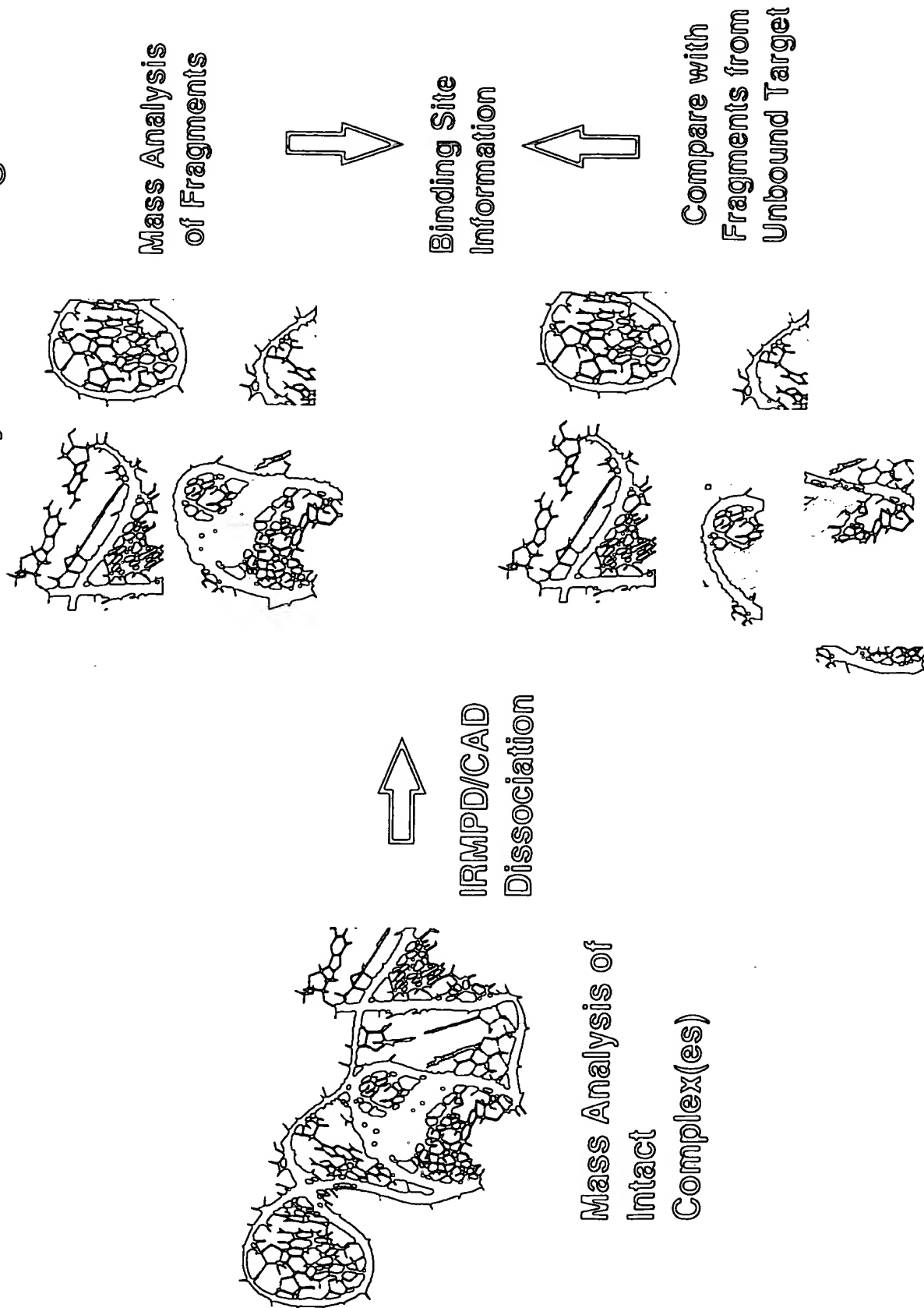


Figure 146

# MASS Analysis of 27 Member Library with 16S A-site RNA

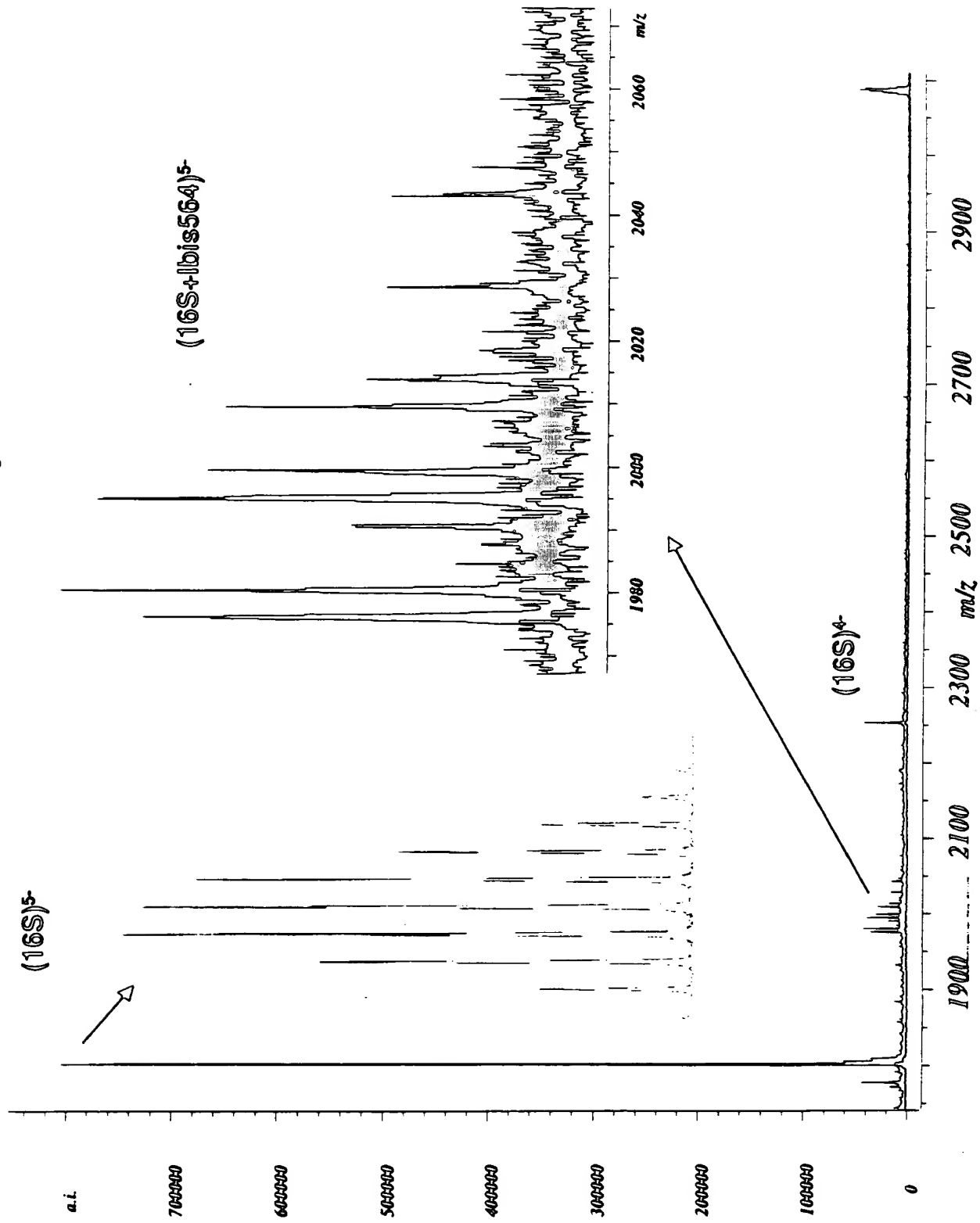
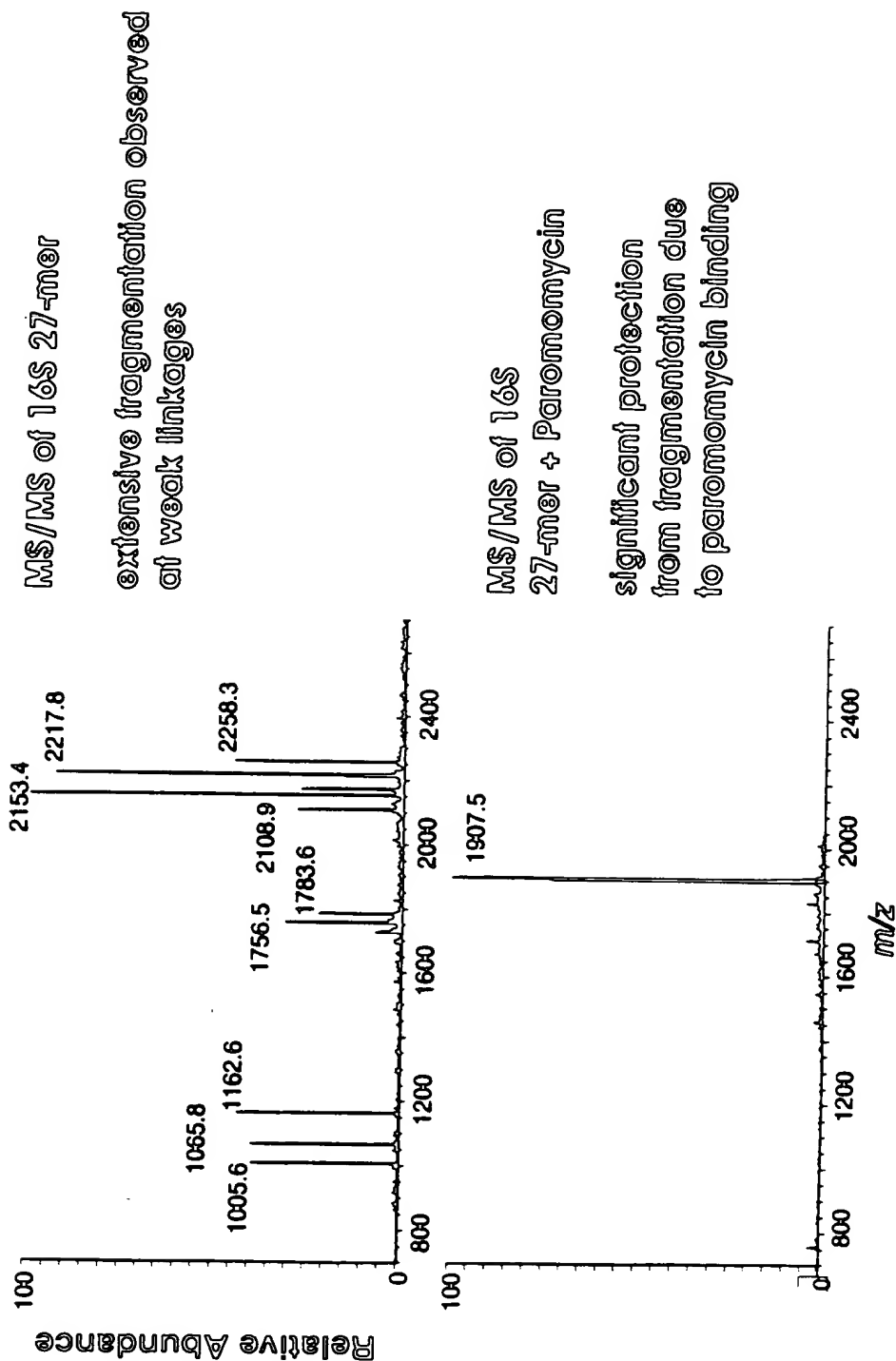


Figure 147

# MASS Protection Assay



**Figure 148**

# MASS Protection Assay

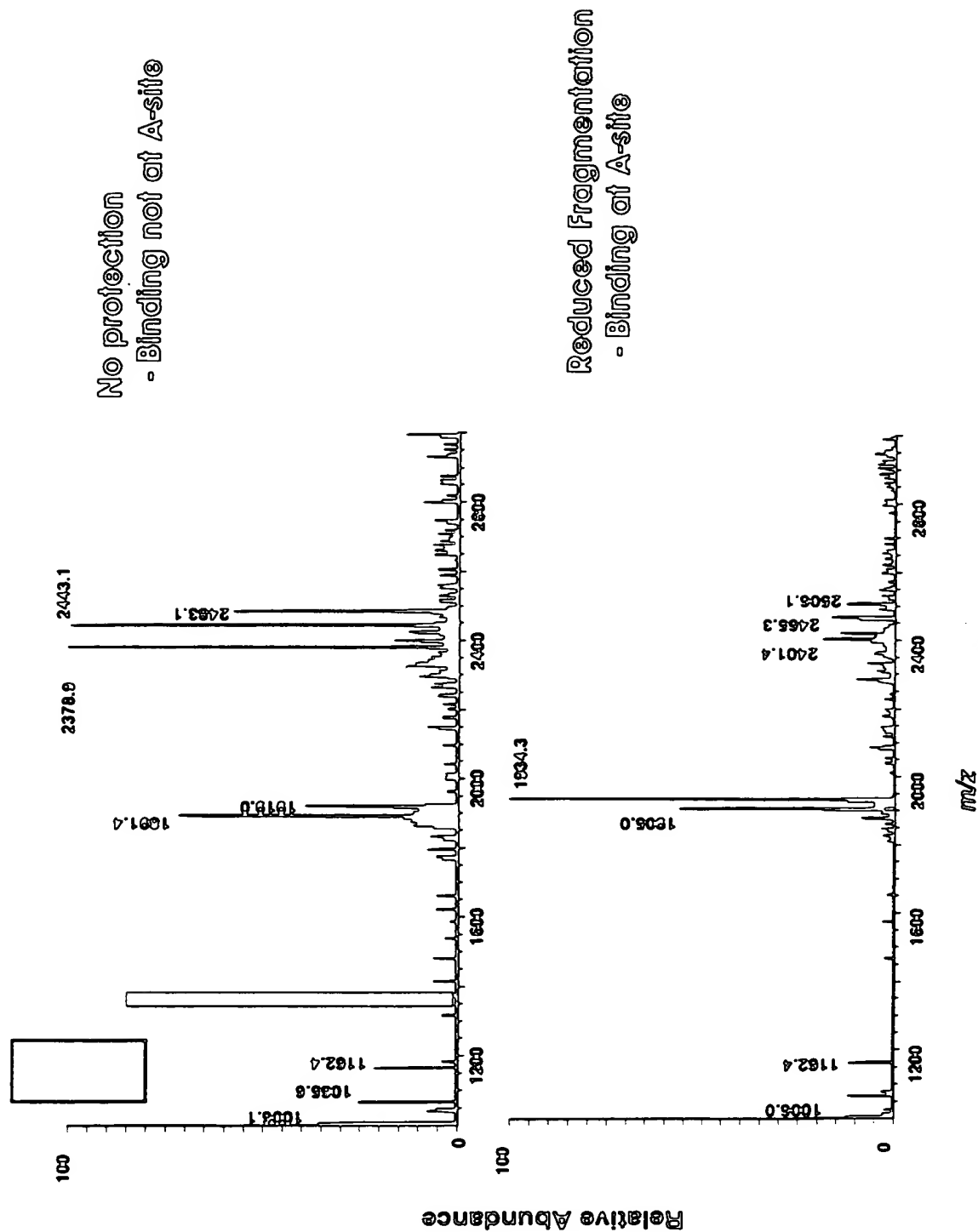
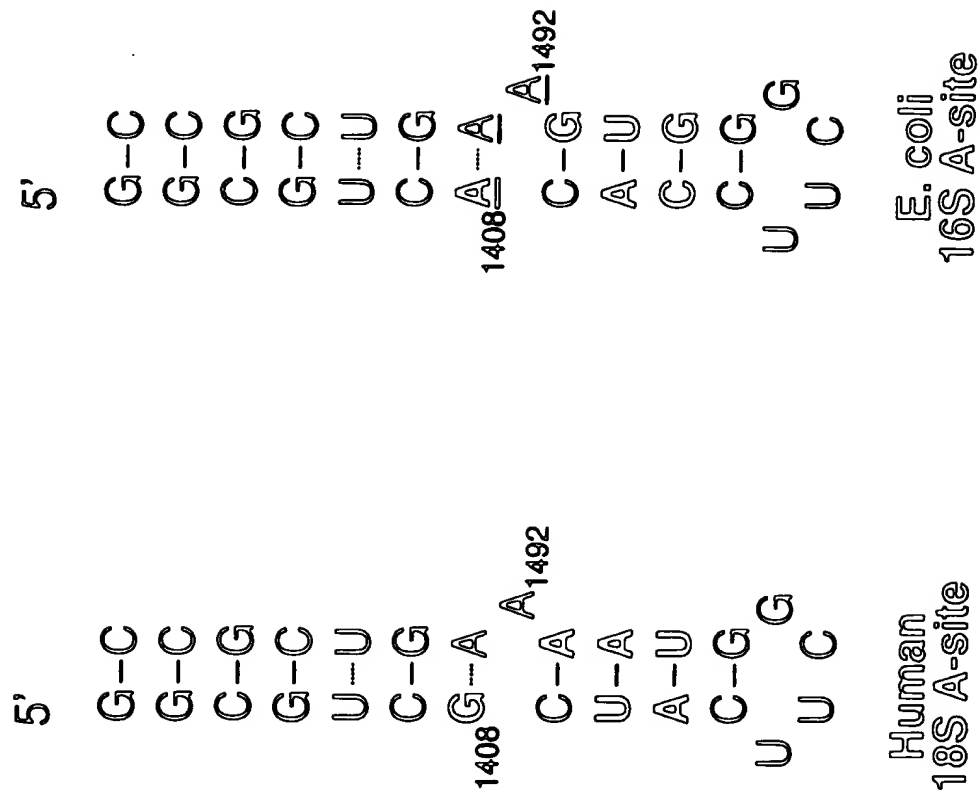


Figure 149

# Eukaryotic and Prokaryotic A-Sites

Aminoglycoside antibiotics bind to

A-site of decoding region in 16S RNA



$\Delta$  MW = 15.011 Da



# Simultaneous Screening of 16S A-site and 18S A-site Model RNAs Against Aminoglycoside Mixture

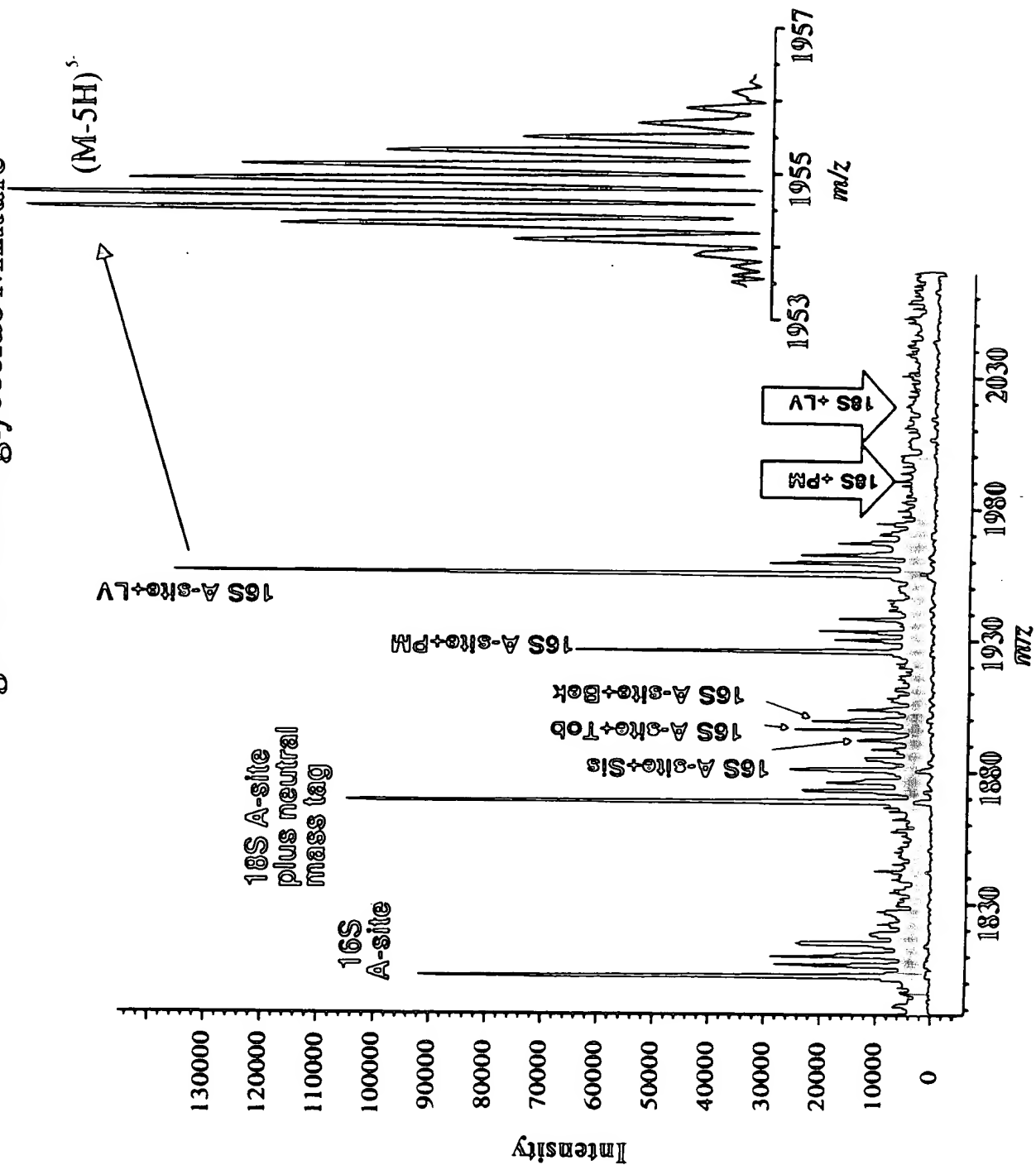




Figure 152

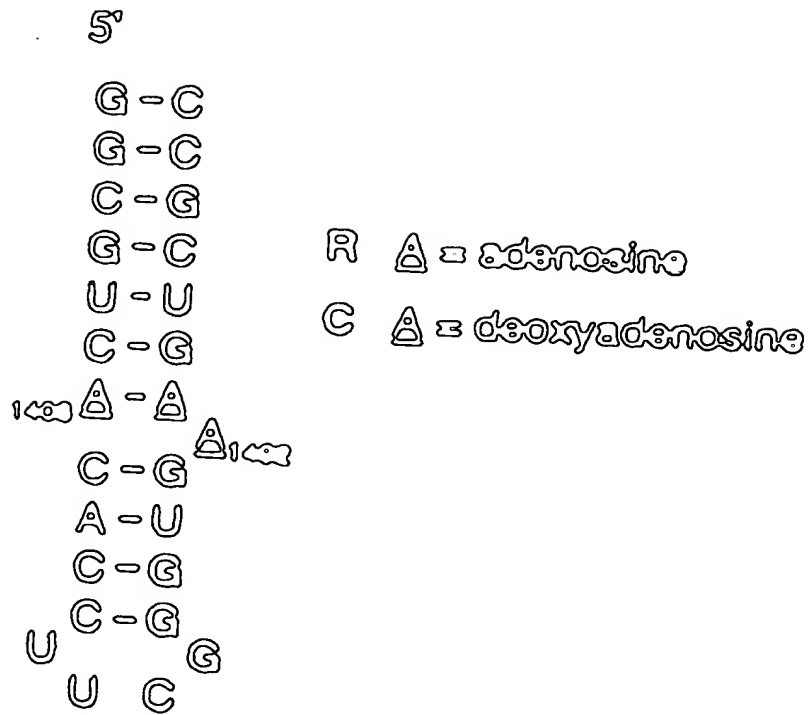


Figure 153

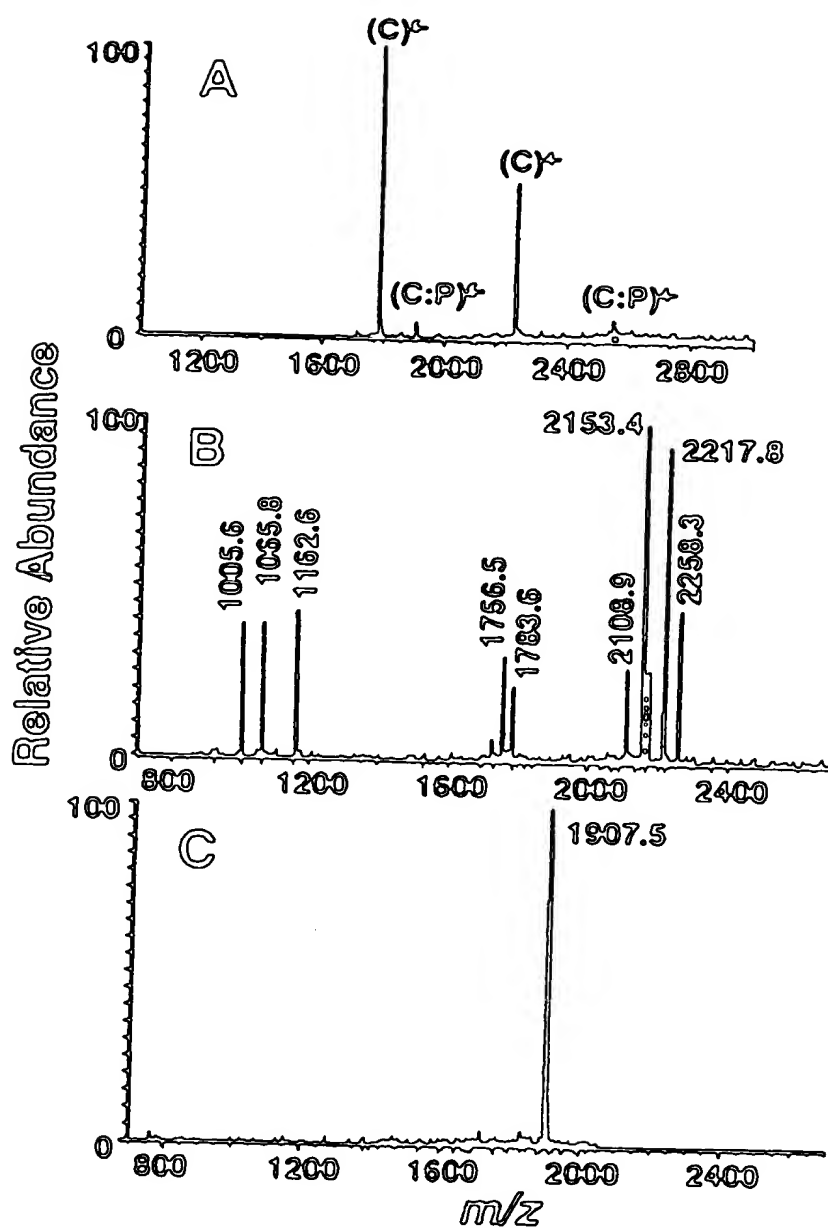
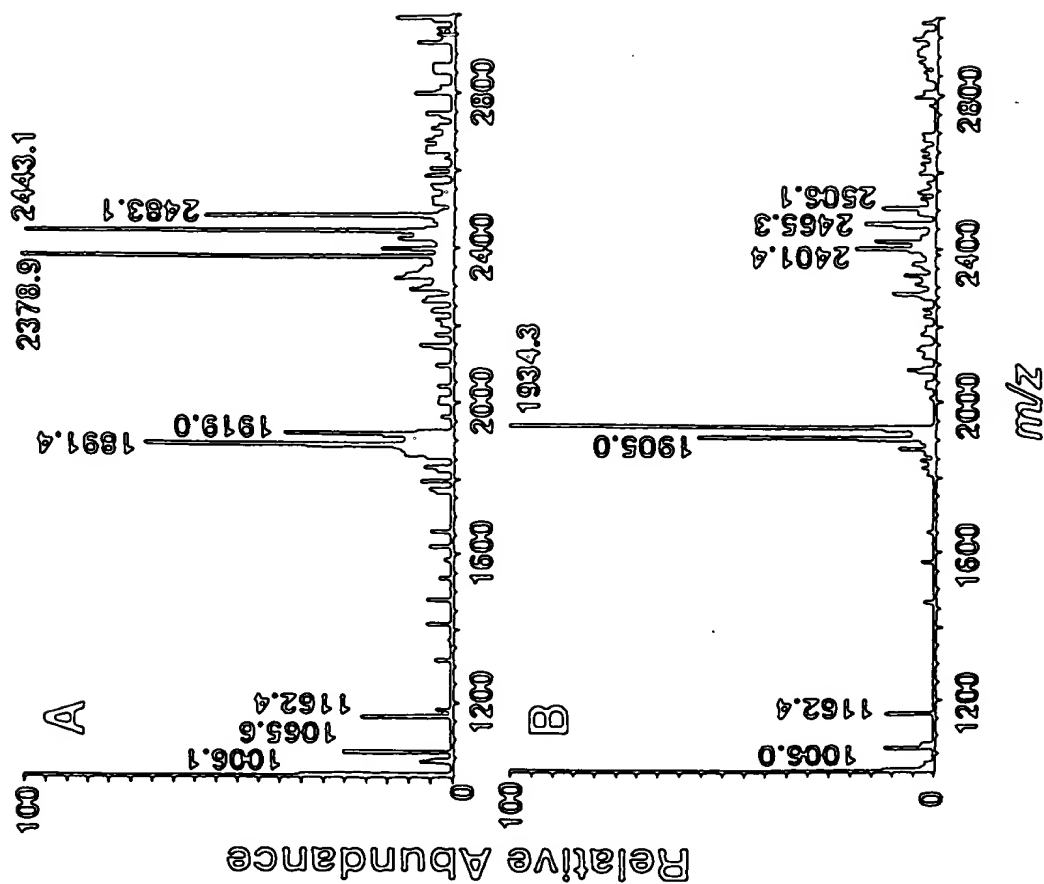


Figure 154



2008.080 : 142.901

Figure 155

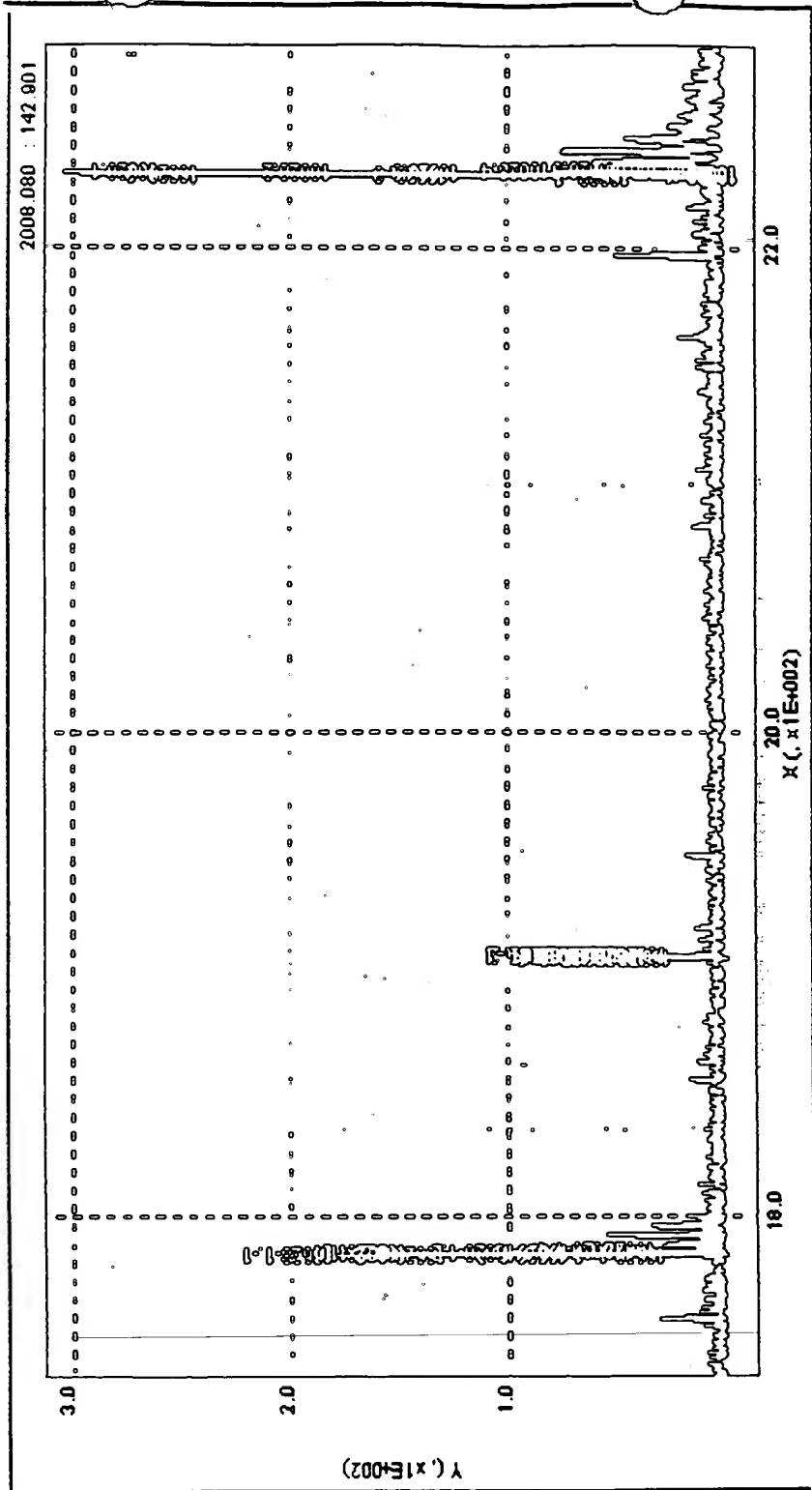




Figure 158

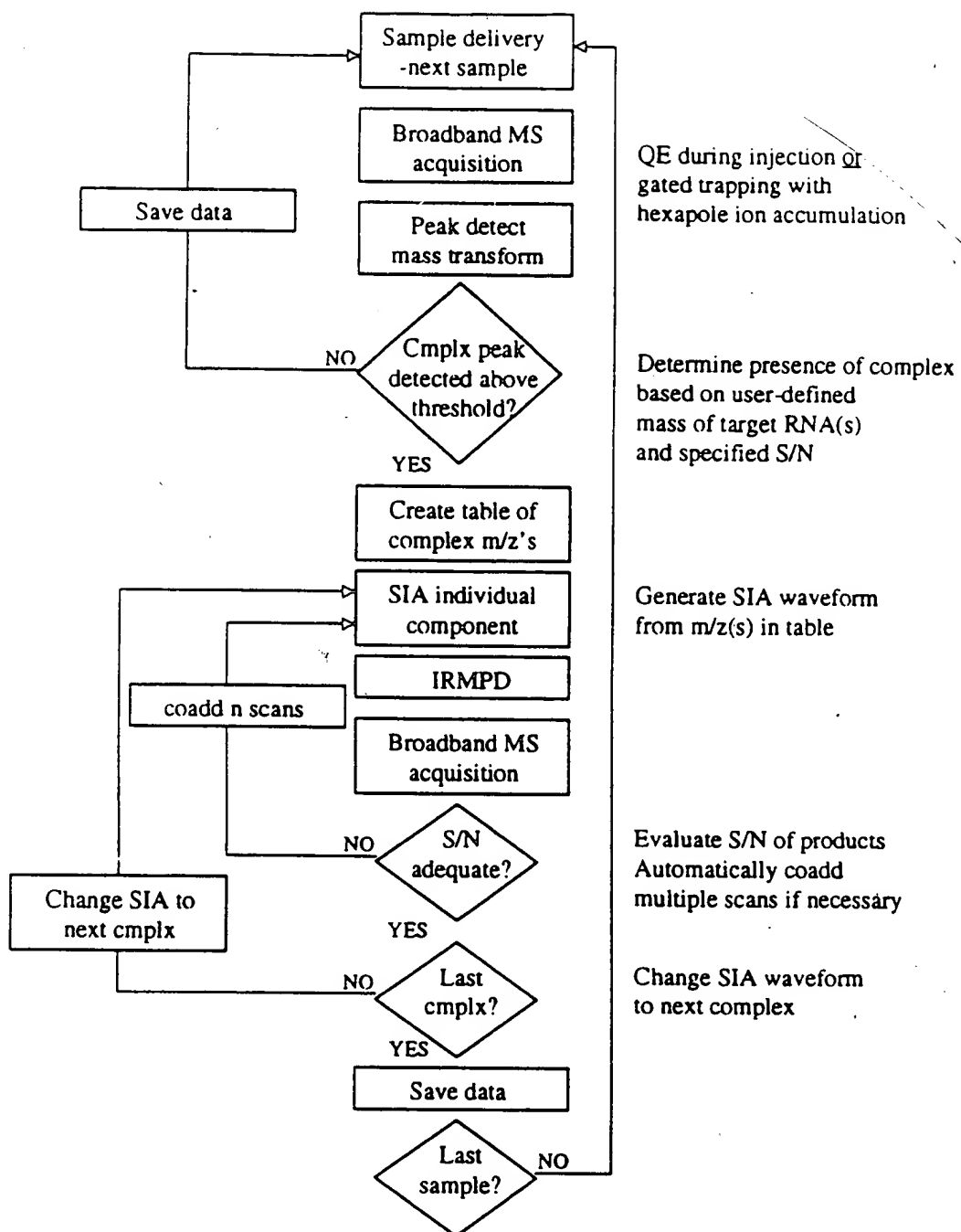


Figure 157

nr	name	apex	start	stop	height	area
1	16628-1-4	1783.710	1783.635	1783.834	14.55	1.63
2	16628-1-3	1783.909	1783.834	1783.972	60.04	5.15
3	16628-1-2	1784.109	1784.021	1784.184	115.60	11.14
4	16628-1-1	1784.308	1784.233	1784.383	167.34	15.89
5	16628-1.0	1784.508	1784.433	1784.620	133.94	14.74
6	16628-1.1	1784.707	1784.620	1784.795	136.60	13.38
7	16628-1.2	1784.907	1784.795	1784.982	82.63	8.56
8	16628-1.3	1785.107	1785.032	1785.219	57.81	5.21
9	16628-1.4	1785.306	1785.232	1785.369	32.31	2.65
10	16628-1.5	1785.506	1785.456	1785.569	17.67	1.12
11	16628.10019-4	1906.974	1906.874	1907.031	12.63	1.00
12	16628.10019-3	1907.173	1907.045	1907.273	22.54	2.11
13	16628.10019-2	1907.373	1907.287	1907.444	33.86	2.91
14	16628.10019-1	1907.572	1907.458	1907.701	34.87	3.30
15	16628.10019.0	1907.772	1907.701	1907.843	20.93	1.55
16	16628.10019.1	1907.972	1907.900	1908.043	21.03	1.55
17	16628.10019.2	1908.157	1908.086	1908.271	10.97	0.90
18	16628-4	2229.874	2229.679	2230.029	27.51	4.87
19	16628-3	2230.146	2230.029	2230.263	111.72	16.23
20	16628-2	2230.380	2230.263	2230.516	225.18	32.39
21	16628-1	2230.633	2230.516	2230.770	280.66	40.90
22	16628.0	2230.887	2230.770	2231.023	287.24	41.95
23	16628.1	2231.140	2231.023	2231.257	242.23	34.17

Graph Table